

```

1 ATGGATTTTC TCCTGGCGCT GGTGCTGGTA TCCTCGCTCT ACCTGCAGGC
51 GGCCGCCGAG TTCGACGGGA GGTGGCCCAG GCAAATAGTG TCATCGATTG
101 GCCTATGTCG TTATGGTGGG AGGATTGACT GCTGCTGGGG CTGGGCTCGC
151 CAGTCTTGGG GACAGTGTCA GCCTTTCTAC GTCTTAAGGC AGAGAATAGC
201 CAGGATAAGG TGCCAGCTCA AAGCTGTGTG CCAACCACGA TGCAAACATG
251 GTGAATGTAT CGGGCCAAAC AAGTGCAAGT GTCATCCTGG TTATGCTGGA
301 AAAACCTGTA ATCAAGACGA GCACATCCCA GCTCCTCTTG ACCAAGGCAG
351 TGAACAGCCT CTTTTCCAAC CCCTGGATCA CCAAGCCACA AGTTTGCCTT
401 CAAGGGATCT AAATGAGTGT GGCCTGAAGC CCCGGCCCTG TAAGCACAGG
451 TGCATGAACA CTTACGGCAG CTACAAGTGC TACTGTCTCA ACGGATATAT
501 GCTCATGCCG GATGGTTCCT GCTCAAGTGC CCTGACCTGC TCCATGGCAA
551 ACTGTCAGTA TGGCTGTGAT GTTGTTAAAG GACAAATACG GTGCCAGTGC
601 CCATCCCCTG GCCTGCAGCT GGCTCCTGAT GGGAGGACCT GTGTAGATGT
651 TGATGAATGT GCTACAGGAA GAGCCTCCTG CCCTAGATTT AGGCAATGTG
701 TCAACACTTT TGGGAGCTAC ATCTGCAAGT GTCATAAAGG CTTGATCTC
751 ATGTATATTG GAGGCAAATA TCAATGTCAT GACATAGACG AATGCTCACT
801 TGGTCAGTAT CAGTGCAGCA GCTTTGCTCG ATGTTATAAC GTACGTGGGT
851 CCTACAAGTG CAAATGTAAA GAAGGATACC AGGGTGATGG ACTGACTTGT
901 GTGTATATCC CAAAAGTTAT GATTGAACCT TCAGGTCCAA TTCATGTACC
951 AAAGGGAAAT GGTACCATTT TAAAGGGTGA CACAGGAAAT AATAATTGGA
1001 TTCCTGATGT TGGGAAGTACT TGGTGGCCTC CGAAGACACC ATATATTCCT
1051 CCTATCATTA CCAACAGGCC TACTTCTAAG CCAACAACAA GACCTACACC
1101 AAAGCCAACA CCAATTCCTA CTCCACCACC ACCACCACCC CTGCCAACAG
1151 AGCTCAGAAC ACCTCTACCA CCTACAACCC CAGAAAGGCC AACCACCGGA
1201 CTGACAACTA TAGCACCAGC TGCCAGTACA CCTCCAGGAG GGATTACAGT
1251 TGACAAACAG GTACAGACAG ACCCTCAGAA ACCCAGAGGA GATGTGTTCA
1301 TTCCACGGCA ACCTTCAAAT GACTTGTTTG AAATATTTGA AATAGAAAGA
1351 GGAGTCAGTG CAGACGATGA AGCAAAGGAT GATCCAGGTG TTCTGGTACA
1401 CAGTTGTAAT TTTGACCATG GACTTTGTGG ATGGATCAGG GAGAAAGACA
1451 ATGACTTGCA CTGGGAACCA ATCAGGGACC CAGCAGGTGG ACAATATCTG
1501 ACAGTGTCGG CAGCCAAAGC CCCAGGGGGA AAAGCTGCAC GCTTGGTGCT
1551 ACCTCTCGGC CGCCTCATGC ATTCAGGGGA CCTGTGCCTG TCATTCAGGC
1601 ACAAGGTGAC GGGGCTGCAC TCTGGCACAC TCCAGGTGTT TGTGAGAAAA
1651 CACGGTGCCC ACGGAGCAGC CCTGTGGGGA AGAAATGGTG GCCATGGCTG
1701 GAGGCAAACA CAGATCACCT TCGGAGGGGC TGACATCAAG AGCGTCGTCT
1751 TCAAAGGTGA AAAAAGGCGT GGTCACTG GGGAGATTGG ATTAGATGAT
1801 GTGAGCTTGA AAAAAGGCCA CTGCTCTGAA GAACGCTAA (SEQ ID NO:1)

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FEATURES:

Start Codon: 1
Stop Codon: 1837

Homologous proteins:

Top 10 BLAST Hits:

	Score	E
CRA 50000098943299 /altid=gi 15795193 /def=ref NP_277060.1 nep...	1190	0.0
CRA 46000103872918 /altid=gi 15128103 /def=gb AAK84391.1 AF3970...	1147	0.0
CRA 84000042916333 /altid=gi 15430248 /def=gb AAK96011.1 (AY03...	1128	0.0
CRA 84000042916331 /altid=gi 15430246 /def=gb AAK96010.1 (AY03...	1084	0.0
CRA 78000201656899 /altid=gi 14763663 /def=ref XP_040394.1 epi...	397	e-109
CRA 163000000492958 /altid=gi 9506563 /def=ref NP_062270.1 EGF...	396	e-109
CRA 157000140328010 /altid=gi 6752658 /def=gb AAF27812.1 AF1860...	396	e-109
CRA 157000140333453 /altid=gi 13124888 /def=ref NP_056322.2 ep...	395	e-109
CRA 1000682328934 /altid=gi 7512796 /def=pir T17324 hypothetical...	385	e-106
CRA 60000046724650 /altid=gi 13929180 /def=ref NP_114014.1 fib...	147	4e-34

FIGURE 1A

Blast hits to dbEST:

<u>CRA Number</u>	<u>gi Number</u>	<u>Score</u>	<u>Expect</u>
CRA 113000119195127	gi 14391046	1068 bits (539)	0.0
CRA 110000024586745	gi 12320908	866 bits (437)	0.0
CRA 87000000737360	gi 7312275	842 bits (425)	0.0
CRA 113000119269070	gi 14399233	831 bits (419)	0.0
CRA 113000119283425	gi 14400823	827 bits (417)	0.0
CRA 113000119283416	gi 14400822	785 bits (396)	0.0
CRA 112000057002060	gi 14377756	680 bits (343)	0.0
CRA 147000029699826	gi 11300389	668 bits (337)	0.0
CRA 117000088322182	gi 12462132	563 bits (284)	1e-157

Expression (Tissue Source):

<u>gi Number</u>	<u>Organ</u>
gi 14391046	head_neck
gi 12320908	nervous_tumor
gi 7312275	head_neck
gi 14399233	head_neck
gi 14400823	head_neck
gi 14400822	head_neck
gi 14377756	colon
gi 11300389	breast_normal
gi 12462132	placenta_normal

FIGURE 1B

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1 MDFLALVLV SSLYLQAAAE FDGRWPRQIV SSIGLCRYGG RIDCCWGWAR
51 QSWGQCQFFY VLRQRIARIR CQLKAVCQPR CKHGECIGPN KCKCHPGYAG
101 KTCNQDEHIP APLDQGSEQP LFQPLDHQAT SLPSRDLNEC GLKPRPCKHR
151 CMNTYGSYKC YCLNGYMLMP DGSCSSALTC SMANCQYGCD VVKGQIRCQC
201 PSPGLQLAPD GRTCDVDVDEC ATGRASCPRF RQCVNTFGSY ICKCHKGFDL
251 MYIGGKYQCH DIDECSLGQY QCSSFARCYN VRGSYKCKCK EGYQGDGLTC
301 VYIPKVMIEP SGPIHVPKGN GTILKGDGTN NNWIPDVGST WWPPKTPYIP
351 PIITNRPTSK PTTRPTPKPT PIPTPPPPP LPTELRTPLP PTTPERPTTG
401 LTTIAPAAST PPGGITVDNR VQTDPOKPRG DVFIQRQPSN DLFEIFEIER
451 GVSADDEAKD DPGVLVHSCN FDHGLCGWIR EKDNLDHWEP IRDPAGGQYL
501 TVSAAKAPGG KAARLVLPLG RLMHSGDLCL SFRHKVTGLH SGTLQVFVRK
551 HGAHGAALWG RGGHGWQRQT QITLRGADIK SVVFKGEKRR GHTGEIGLDD
601 VSLKKGHCSE ER (SEQ ID NO:2)

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FEATURES:

Functional domains and key regions:

Prosite results:

PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

320-323 NGTI

PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 10

1	157-159	SYK
2	222-224	TGR
3	284-286	SYK
4	354-356	TNR
5	358-360	TSK
6	362-364	TTR
7	366-368	TPK
8	531-533	SFR
9	573-575	TLR
10	602-604	SLK

PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 3

1	213-216	TCVD
2	392-395	TTPE
3	453-456	SADD

PDOC00007 PS00007 TYR_PHOSPHO_SITE

Tyrosine kinase phosphorylation site

246-252 KGFDLMY

PDOC00008 PS00008 MYRISTYL

N-myristoylation site

Number of matches: 10

1	156-161	GSYKCY
2	172-177	GSCSSA
3	194-199	GQIRCQ
4	238-243	GSYICK
5	268-273	GQYQCS
6	283-288	GSYKCK
7	497-502	GQYLTV
8	509-514	GGKAAR
9	538-543	GLHSGT
10	552-557	GAHGAA

FIGURE 2A

PDOC00010 PS00010 ASX_HYDROXYL
 Aspartic acid and asparagine hydroxylation site
 Number of matches: 3

1	151-162	CMNTYGSYKCYC
2	233-244	CVNTFGSYICKC
3	278-289	CYNVRGSYKCKC

PDOC00016 PS00016 RGD
 Cell attachment sequence
 429-431 RGD

PDOC00021 PS00022 EGF_1
 EGF-like domain signature 1
 92-103 CKCHPGYAGKTC

PDOC00021 PS01186 EGF_2
 EGF-like domain signature 2
 Number of matches: 3

1	92-103	CKCHPGYAGKTC
2	160-174	CYCLNGYMLMPDGSC
3	287-300	CKCKEGYQGDGLTC

PDOC00913 PS01187 EGF_CA
 Calcium-binding EGF-like domain signature
 Number of matches: 3

1	136-160	DLNECGLKPRPCKHRCMNTYGSYKC
2	216-242	DVDECATGRASCPFRQCVNTFGSYIC
3	261-287	DIDECSLGQYQCSSFARCYNVRGSYKC

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	3	23	0.942	Putative
2	163	183	0.765	Putative
3	397	417	1.209	Certain

SignalP results:

< Is the sequence a signal peptide?

#	Measure	Position	Value	Cutoff	Conclusion
	max. C	20	0.657	0.37	YES
	max. Y	20	0.713	0.34	YES
	max. S	6	0.960	0.88	YES
	mean S	1-19	0.901	0.48	YES

Most likely cleavage site between pos. 19 and 20: AAA-EF

FIGURE 2B

BLAST Alignment to Top Hit:

>CRA|50000098943299 /altid=gi|15795193 /def=ref|NP_277060.1|
nephronectin [Mus musculus] /org=Mus musculus
/taxon=10090 /div=ROD /dataset=nraa /length=609
Length = 609

Score = 1190 bits (3045), Expect = 0.0

Identities = 536/610 (87%), Positives = 569/610 (92%), Gaps = 3/610 (0%)

Query: 1 MDLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
M LLA VL SLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY
Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGECIGPNKCKCHPGYAGKTCNQDEHI-PAPLDQGSEQ 119
VLRQR+ARIRCQLKAVCQP+CKHGEC+GPNKCKCHPG+AGKTCNQDE P PLDQGSEQ
Sbjct: 61 VLRQLARIRCQLKAVCQPQCKHGECVGNKCKCHPGFAGKTCNQDESFHPTPLDQGSEQ 120

Query: 120 PLFQPLDHOATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALT 179
PLFQP DHQAT++PSRDLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGSCSSAL+
Sbjct: 121 PLFQPPDHQATNVPSPRDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGSCSSALS 180

Query: 180 CSMANCQYGCDDVVGQIRQCQSPGLQLAPDGRTCDVDECATGRASCPFRFRQCVNTFGS 239
CSMANCQYGCDDVVGQ+RCQCQSPGLQLAPDGRTCDV+DECATGR SCPRFRQCVNTFGS
Sbjct: 181 CSMANCQYGCDDVVGQVRCQCQSPGLQLAPDGRTCDVIDECATGRVSCPRFRQCVNTFGS 240

Query: 240 YICKCHKGFGLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLT 299
YICKCH GFDLMYIGGKYQCHDIDECSLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL
Sbjct: 241 YICKCHTGFGLMYIGGKYQCHDIDECSLGQHQCSSYARCYNIHGSYKCQCRDGYEGDGLN 300

Query: 300 CVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNWIPDVGSTWWPPKTPYIPPIITNRPTS 359
CVYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTS
Sbjct: 301 CVYIPKVMIEPSGPIHMPERNGTISKDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTS 360

Query: 360 KPTTRPTPKPTPIPTPPPPPLPTELRT-PLPPTTPERPTTGLTTIAPAASTPPGGITVD 418
KPTTRPTP PTP PTPPPPPPLPTE RT PLPPT PERP+T TTIAPA ST ITVD
Sbjct: 361 KPTTRPTPNPTPQPTPPPPPPPLPTEPRPTPLPPT-PERPSTRPTTIAPATSTTTTRVITVD 419

Query: 419 NRVTQDPQKPRGDFVFIQRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGW 478
NR+QTDPQKPRGDFVFIQRQP+NDLFEIFEIERGVSAD+E KDDPG+L+HSCNFDHGLCGW
Sbjct: 420 NRIQTDPQKPRGDFVFIQRQPTNDLFEIFEIERGVSADDEEVKDDPGILIHSCNFDHGLCGW 479

Query: 479 IREKDNLDLHWEPIRDPAGGQYLTVSAAPGGKAARLVLPGLRLMHSGDLCLSFRHKVGTG 538
IREKD+DLHWE RDPAGGQYLTVSAAPGGKAARLV LG LMHSGDLCLSFRHKVGTG
Sbjct: 480 IREKDSLDLHWETARDPAGGQYLTVSAAPGGKAARLVLRGLHLMHSGDLCLSFRHKVGTG 539

Query: 539 LHSGLTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGL 598
LHSGLTLQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGL
Sbjct: 540 LHSGLTLQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKSIVFKGEKRRGHTGEIGL 599

Query: 599 DDVSLKKGHC 608
DDVSLK+G C
Sbjct: 600 DDVSLKRGRC 609 (SEQ ID NO:4)

FIGURE 2C

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>CRA|46000103872918 /altid=gill15128103 /def=gb|AAK84391.1|AF397007_1
(AF397007) nephronectin [Mus musculus] /org=Mus musculus
/taxon=10090 /div=ROD /dataset=nraa /length=592
Length = 592

Score = 1147 bits (2934), Expect = 0.0
Identities = 520/610 (85%), Positives = 552/610 (90%), Gaps = 20/610 (3%)

Query: 1 MDLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
M LLA VL SSLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQP
Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQP-- 58

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGECIGPNKCKCHPGYAGKTCNQDEHI-PAPLDQGSEQ 119
VCQP+CKHGEC+GPNKCKCHPG+AGKTCNQDE P PLDQGSEQ
Sbjct: 59 -----VCQPQCKHGECVGPKNCKCHPGFAGKTCNQDESFHPTPLDQGSEQ 103

Query: 120 PLFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALT 179
PLFQP DHQAT++PSRDLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGSCSSAL+
Sbjct: 104 PLFQPPDHQATNVPSRDLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGSCSSALS 163

Query: 180 CSMANCQYGCDVVKQGQIRCQCPSPGLQLAPDGRTCVDVDECATGRASCPFRFRQCVNTFGS 239
CSMANCQYGCDVVKGQ+RCQCPSPGLQLAPDGRTCVD+DECATGR SCPRFRQCVNTFGS
Sbjct: 164 CSMANCQYGCDVVKGQVRCQCPSPGLQLAPDGRTCVDIDECATGRVSCPRFRQCVNTFGS 223

Query: 240 YICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVGRGSYKCKCKEGYQGDGLT 299
YICKCH GFDLMYIGGKYQCHDIDECSLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL
Sbjct: 224 YICKCHTGFDLMYIGGKYQCHDIDECSLGQHQCSSYARCYNIHGSYKQCRDGYEGDGLN 283

Query: 300 CVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNWIPDVGSTWWPPKTPYIPPIITNRPTS 359
CVYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTS
Sbjct: 284 CVYIPKVMIEPSGPIHMPERNGTISKGDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTS 343

Query: 360 KPTTRPTPKPTPIPTPPPPPLPTELRT-PLPPTTPERPTTGLTTIAPAASTPPGGITVD 418
KPTTRPTP PTP PTPPPPPPLPTE RT PLPPT PERP+T TTIAPA ST ITVD
Sbjct: 344 KPTTRPTPNPTPQPTPPPPPPPLPTEPRTTPLPPT-PERPSTRPTTIAPATSTTTTRVITVD 402

Query: 419 NRVTQDPQKPRGDFVFIQRQPSNDLFEIFEIERGVSADDEAKDDPGVLVHSCNFDHGLCGW 478
NR+QTDPQKPRGDFVFIQRQ+NDLFEIFEIERGVSAD+E KDDPG+L+HSCNFDHGLCGW
Sbjct: 403 NRIQTDPQKPRGDFVFIQRQPTNDLFEIFEIERGVSADDEEVKDDPGILIHSCNFDHGLCGW 462

Query: 479 IREKDNLDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFRHKVTG 538
IREKD+DLHWE RDPAGGQYLTVSAAKAPGGKAARLV LG LMHSGDLCLSFRHKVTG
Sbjct: 463 IREKDSLDLHWETARDPAGGQYLTVSAAKAPGGKAARLVRLGLHMHSGDLCLSFRHKVTG 522

Query: 539 LHSGLTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGL 598
LHSGLTLQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGL
Sbjct: 523 LHSGLTLQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKSIVFKGEKRRGHTGEIGL 582

Query: 599 DDVSLKKGHC 608
DDVSLK+G C
Sbjct: 583 DDVSLKRGRG 592 (SEQ ID NO:5)

```

FIGURE 2D

>CRA|84000042916333 /altid=gi|15430248 /def=gb|AAK96011.1|
 (AY035899) nephronectin long isoform [Mus musculus]
 /org=Mus musculus /taxon=10090 /div=ROD /dataset=nraa
 /length=578
 Length = 578

Score = 1128 bits (2885), Expect = 0.0
 Identities = 512/609 (84%), Positives = 543/609 (89%), Gaps = 32/609 (5%)

Query: 1 MDLLALVLVSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60
 M LLA VL SLYLQ AA+FDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY
 Sbjct: 1 MAVLLAAVLASSLYLQVAADFGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPFY 60

Query: 61 VLRQRIARIRCQLKAVCQPRCKHGECIGPNKCKCHPGYAGKTCNQDEHIPAPLDQGSEQP 120
 VLRQR+ARIRCQLKAVCQP+CKHGEC+GPNKCKCHPG+AGKTCNQ
 Sbjct: 61 VLRQLARIRCQLKAVCQPQCKHGECVGNKCKCHPGFAGKTCNQ----- 105

Query: 121 LFQPLDHQATSLPSRDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPDGSCSSALTC 180
 DLNECGLKPRPCKHRCMNT+GSYKCYCLNGYML+PDGSCSSAL+C
 Sbjct: 106 -----DLNECGLKPRPCKHRCMNTFGSYKCYCLNGYMLLPDGSCSSALSC 150

Query: 181 SMANCQYGCDVVKGQIRQCQPSGLQLAPDGRTCVDVDECATGRASCPFRQCVNTFGSY 240
 SMANCQYGCDVVKGQ+RCQCPSPGLQLAPDGRTCVD+DECATGR SCPRFRQCVNTFGSY
 Sbjct: 151 SMANCQYGCDVVKGQVRCQCPSPGLQLAPDGRTCVDIDECATGRVSCPRFRQCVNTFGSY 210

Query: 241 ICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQGDGLTC 300
 ICKCH GFDLMYIGGKYQCHDIDECSLGQ+QCSS+ARCYN+ GSYKC+C++GY+GDGL C
 Sbjct: 211 ICKCHTGFDLMYIGGKYQCHDIDECSLGQHQCSSYARCYNIHGSYKCCQCRDGYEGDGLNC 270

Query: 301 VYIPKVMIEPSGPIHVPKNGTILKGDGTGNWNWIPDVGSTWVPPKTPYIPPIITNRPTSK 360
 VYIPKVMIEPSGPIH+P+ NGTI KGD G+ N IPD GST WP KTPYIPP+ITNRPTSK
 Sbjct: 271 VYIPKVMIEPSGPIHMPERNGTISKGDGGHANRIPDAGSTRWPLKTPYIPPVITNRPTSK 330

Query: 361 PTTRPTPKPTPIPTPPPPPLPTELRL-TPLPPTTTPERTTGLTTIAPAASTPPGGITVDN 419
 PTTRPTP PTP PTPPPPPPLETE R TPLPP TPERP+T TTIAPA ST ITVDN
 Sbjct: 331 PTTRPTPNPTPQPTPPPPPLPTEPRTTPLPP-TPERPSTRPTTIAPATSTTTTRVITVDN 389

Query: 420 RVQTDQKPRGDVFI PRQPSNDLFEIFEIERGVSADEAKDDPGVLVHSCNFDHGLCGWI 479
 R+QTDQKPRGDVFI PRQP+NDLFEIFEIERGVSADE+KDDPG+L+HSCNFDHGLCGWI
 Sbjct: 390 RIQTDQKPRGDVFI PRQPTNDLFEIFEIERGVSADEEVKDDPGILIHSCNFDHGLCGWI 449

Query: 480 REKDNDLHWEPIRDPAGGQYLTVSAAKAPGGKAARLVLPGLRLMHSGDLCLSFRHKVTGL 539
 REKD+DLHWE RDPAGGQYLTVSAAKAPGGKAARLV LG LMHSGDLCLSFRHKVTGL
 Sbjct: 450 REKSDLHWETARDPAGGQYLTVSAAKAPGGKAARLVRLGLHLMHSGDLCLSFRHKVTGL 509

Query: 540 HSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQITLRGADIKSVVFKGEKRRGHTGEIGLD 599
 HSGTLQVFVRKHG HGAALWGRNGGHGWRQTQITLRGAD+KSV+FKGEKRRGHTGEIGLD
 Sbjct: 510 HSGTLQVFVRKHGTHGAALWGRNGGHGWRQTQITLRGADVKSIVFKGEKRRGHTGEIGLD 569

Query: 600 DVSLKKGHC 608
 DVSLK+G C
 Sbjct: 570 DVSLKRGRC 578 (SEQ ID NO:6)

FIGURE 2E

Hmmer search results (Pfam):

Scores for sequence family classification (score includes all domains):

Model	Description	Score	E-value	N
CE00409	E00409 fibulin	108.3	3.8e-30	3
PF00629	MAM domain.	88.2	1.7e-22	1
PF00008	EGF-like domain	68.0	1.7e-17	5
CE00283	E00283 selectin	13.0	0.014	2
PF01278	Ompin family	1.9	6.6	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
PF00008	1/5	77	103 ..	1	45 {}	17.3	0.0036
CE00283	1/2	74	105 ..	119	153 ..	10.7	0.059
PF00008	2/5	140	172 ..	1	42 {}	19.4	0.00091
PF00008	3/5	180	214 ..	1	45 {}	19.0	0.0012
CE00409	1/3	136	227 ..	415	514 ..	69.4	4.5e-19
CE00283	2/2	226	248 ..	124	146 ..	8.7	0.2
PF00008	4/5	220	249 ..	1	41 {}	10.8	0.25
CE00409	2/3	232	273 ..	429	473 ..	35.2	2.3e-09
CE00409	3/3	277	298 ..	344	365 ..	16.3	0.00053
PF00008	5/5	265	300 ..	1	45 {}	31.7	2.9e-07
PF01278	1/1	477	493 ..	241	257 ..	1.9	6.6
PF00629	1/1	469	610 ..	1	170 {}	88.2	1.7e-22

FIGURE 2F

1 GAGAAAATTG AGATTACTAC CTGCAAGGTG TCATTACCTG GTAAGAAGCC
 51 TATCAAAAGT TTGTCTCCT GAAAAAGTAG TTATTGCTAA AAGCTAGCTG
 101 TTTTGATCTC ATTCTTGCTC ATTTGTTTTT AAGACTGAGA TAATGAAATG
 151 TCAC'TCCCAT GGCAACTCTG CCTCTTTTTC GGAATGATCA TTGGTGGTCA
 201 TAGTTGCAGC ATAATAACCA GTTAGACCTT GGAAATCCTT TAGATTCTCC
 251 TTAT'TCCATG ATTTAACAAA GACTGATATA ATTAGCTACA TTTTACTGAA
 301 GGGAGAAGCT AAAGTTCACA GGCAGAATTC AATTTAATCC AATCCATCTG
 351 TTTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNCT ATTGGTTAGA
 451 CTAATGTCTC ACGGGACCCA GAGTGGTAGG GAGGCAATGA CAACACAATA
 501 CATTAAGAGC TACCTTAGAG CATGCTAAGT GTAATAGAAG TATATAAAAC
 551 ACTAGTCTCA GCCAATCAAA AAGTCAGAAA AGGCTTCCTG GGGGACTGTC
 601 GGCTAAATTT AAAC'TCAAA GGTAAAGGGA GATTGTCCAA ATGAAGAAGG
 651 AAGAGGAATG AAGAGGAGGC TAAATTTAAA TGAAGAAGGA GTGTTTTCTA
 701 GGCCAAAGCA AATATATGGA AAACAAAAGA AAGACGCATG TAGATGGGGC
 751 ATTACACTTT TCCCTCCAGT TATTTATCCT GTTTTCATCC ACCACTCTTC
 801 GTCTTTTCTC TAGATCTCCA GTTTTTTAGC CGTATATTAC CCCCTTTCTC
 851 TCTAATCATC CATTGCACAC AGTGAGGTTT ATTTGTAAAT CTAACCCAGG
 901 CACCAACTAA CCAACCAACA AACAAAAACA GCTAAGGAGT AGCCACTGGA
 951 ACCTGGAACC ATGCCTACAC TTACAAAAAT TTGATTTTCT GCAGAAAAAA
 1001 TATTTTGA'CT CCTACATTTT TGGACTTCAT TAGAAGGACC TGAATGGAT
 1051 GACACCAAGC TGTTTGCCTA AAATAATGTC CCAAGCCTGA ATTGGCATGG
 1101 ATCTTTCTTG AGATTA'AAAT AGAAACTTGT TTGCTAACT GAAAACAACT
 1151 TAGAAATCAA AGAGCCATTT AAGTTGAAAC CAT'TATTTT CCTTTCCTTG
 1201 AAGAAAATTC CTGTTTTTAC ACACACTGAA TGATCAGGAT AGTGAATCAC
 1251 CCTACCACAG AACTTTCCAT TAAAAATTTG AAGTTGTAGA AACCTCAAAA
 1301 AGAAAAATGAA GATGGGGGGA AAACGTTTGT AATGTAGCAA ATGANNNNNN
 1351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 1851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNAGATG ATCACTGCAC
 1901 AAGGCTGTCA TTCGAGGTAA GGT'TGGGAAG AGGGGTGACT TGATTGGGCT
 1951 CATGTACATC TTAGGATAAT CATGTTTTCA TTTGAACACA GTCATTTAGT
 2001 ACAATACTTT T'ACTCTGCA ACAACTGAAC AATGATTACT TAAAATGGTT
 2051 TCTAAGTGAT CCCCTCAAGA TCAGGCACCA CAACACTACT AGGCAGTAGC
 2101 AGCCCTTCCT CTCTGGCAGG CACTCATCCC TAGAGGGGCA GTCCTGTCCT
 2151 AATGTGCTCG GGAGTTGAGC TGATAGAGAC AGAAACAGTC TGCTCATTTC
 2201 TTCTTCAAAA CCGACTGGA GAGCCAAATA TTTCTTTTGG TTAGTTACAA
 2251 AATAAAAAAT ATGCCTTTGC CAACTCTGCG GGAAAAGCAA ACTCCCAGAG
 2301 TTTGCCTTCG CTAATTTGTC CAAGTCGTGC TGTGGTTTTA GTAAATGCAG
 2351 AC'ACTGCTCA GCTCCAGCCC CATAAACCTC TCTGCTCTAG GGCTTCTCCG
 2401 CCCTCCGGTG AAAGCTACTG CTCGCCCTCG CAGTCACCAC CTGTT'CGGGC
 2451 GGAACCTGCG GAGCGTGCAC CTACGCCTCG GGCTCCTTTC CTCCTCCACT
 2501 CCCCTTTCCT GCTGGGCACC CTGCTTTCCC TCTCCCAGAG AGGGTTTGCA
 2551 ACTTTTCTCC CAGGCTGGGG CTCGCCCTGC TTGGCTAACC CCAAGAGCC
 2601 ACTGCCGTCC CGCAGCGCCC CTGCCCCCGA GTTGCTGCC CCGCTGGGCC
 2651 CCCGGGAGGA GCGGAGCGCG CTCACCCTTC GCCCGGGGCT GGGAGGGCGG
 2701 CGAGTCGGGC GCACGCGCAC CCCCTGCCCC CCCCTGGCGC CCCTCCCCGC
 2751 GGGCGGTGCA GCTACCCCTG CAGCGCCTCC C'TAGCTAGA AGGGAGCGGG
 2801 AGGGGGCTCC GGGCGCCGCG CAGCAGACCT GCTCCGGCCG CGCGCCTCGC
 2851 CGCTGTCTC CGGGAGCGGC AGCAGTAGCC CGGGCGGCGA GGGCTGGGGG
 2901 TTCCTCGAGA CTCTCAGAGG GGCGCCTCCC ATCGGCGCCC ACCACCCCAA
 2951 CCTGTTCTC GCGGCCCACT GCGTGCGCC CCAGGACCCG CTGCCCAACA

FIGURE 3A

3001 TGGATTTTCT CCTGGCGCTG GTGCTGGTAT CCTCGCTCTA CCTGCAGGCG
3051 GCCGCCGAGT TCGACGGGAG GTGAGCTGGG CCCCGGGGCG CCTCTCCTC
3101 CTTCCCGCGC TAATTTTACA CTCACTGTCT TGGGTCACTT TTTCCCGCGG
3151 GGTTCCTGG TCAGAGAGGC GTCTCTCCA TCCAGAAGTT GGGCCACCGC
3201 ACAGCGTGGC GCGAGGAGAG CGGTCCAGCG GCTCCGAGTG CCCGCCGAG
3251 GCGGAGAGGG CGCGCCCTTG CGAGTCTGGG ACCCATCCG CGGCCCCCCG
3301 AGGGCGACTC GCCCCGGCTC GGAATTAGG ACTGAGGGAG AGGAGCCGCT
3351 GGAGCTGGG ATCTCGGCTC TGAGGGCGCG GTTAGCCAC CTACGCCGAG
3401 GTGACGCGCG AAACATCCCT TACCCGGGAA ACTCCCGCGC CTGAAGTAGA
3451 CGGCTCTTCA CTGGGGAAGC TTCCAGGCCC CGGGGGGAG GCCCGGGCTC
3501 TGCTCAGGGC TCTCGGGGCC GCTCACACAG AGAGTGGGTG CGAGTCAGCG
3551 ACTGGGCTAC GGGGAGATT TGTGGGCTC TCCATTTGGT TTTCTTGAGG
3601 GAAGGAGACT CAAATGAGG ACCGAGGGT GGGCGCTCCG TGAATGTGAG
3651 CATGAGTGTG TGGATGTGTG TGTGAGAGCG CACACACTGC GCCGCTCCTC
3701 AGACTCGGGC GAGCCTGACG GCGGCGTGCT GTGACAGGTT CCAACAACCT
3751 CGGGCGCGCT TCCGCTGTC ACTCAGCCGG TCCTCCCGCG CTCGGGGGCC
3801 GCTCCGGTGT GTGAGAGACA CTGGGTCTGT CGGGAGGGTG TGCTCGGTCC
3851 CCCTCACCTC TGTGCAATTA CAGACTAGGC TCGTCCCGGG TGCAGATGGC
3901 TGCTGCGAAA AGAGTTTTTA CTCTGGCGCA CACCGTCGCC CGGTGCGCTT
3951 CCTTCAGCGA CCTTGCCCC CACCCCTCCG TGAGGTCCC TGCCTAGTCC
4001 TAAAGAAAG TGCCGCACCT GTTTTACCTT TAATCTTGA ACGAATCAAT
4051 TCCACAATTG ATTCGCTTTC TTGTACCCGG AGGCGAACGG AGGGGAACCA
4101 GTGGAGCGCC AAAAGATGTC TAAAACAGCA AATTAAAATG TTGATACCCA
4151 AAATAGAAAG TTCGGGGTTA TTTTGTACTT TGGGCTGGG GGTAGAAAGG
4201 CAGGTAAAAG AAAAGGGGAA TTGAAAAAGA TAAGGAGACT TTAAGAAAAC
4251 GTGATAGCAG CCAGAGTGTA GACCTTTTTT TTTTATTTTT AAAAGCAATT
4301 CTGTGCTCAC ATTTGGGTAT GTTATGCATT TCTTGCACAC ATATTTGCAA
4351 CAAGAAACCC ATCACAAGAT ATGCATATGA TGTGAATGCA TATAGCTTTT
4401 TGTAACTTTA AAAAGATGTC TAAAACAGCA AATTAAAATG TTGATACCCA
4451 GAGGAAAAAA GTCATTTAGG TGTGACTCTA AACAAGGAAA CAATTTAGCA
4501 AATAATGTGT CAACGTGTAA TCAGGTGGAT AAATCTGTAT CCTGAAATTA
4551 CTTTCTTTAG GCATTATTTA CATTAGAGAG GAAAATACTA TGAATTGTTG
4601 ATCTAAGCAC GTTTCAAACC ACAAGGATAC TTGAGATATC AGCTACACTT
4651 TAACTCTCC TTGGTTTTAT TTAGACTTTT TTCTAGTACT TTTTGTGTTT
4701 TTTTGTGTTT GCCACAGTTA TGTCTCAAAA AGAGCTCTGT TACACTTGAT
4751 TTTTGAGAAA CCTTCTGCT CCTTCCCCCA TCCACCTTTT ATATGAGGCA
4801 GAAATTTTTT CTGCTTTGAC ATGTCTTACT TAATACTTTT CAGTTTATGG
4851 TGAATCAGTC AAACCTGGCT TTCACCCAG TAACAGGTGT GGGTCTTTGA
4901 GGAATCTGTT TTATTTCAAG CTTCAGAAAC TATCCTGTGA GTGGCAGCCT
4951 TGAGAAATGT TGGTGTAGC TGGTGCTATT TCTACTAAG AAAGCATCTT
5001 TCCCTCCCGT TTTTCTCCT ACCCTTGTGT GTTGGGGGAT GGGGTATTTA
5051 ACTGTCTGAA ATTTGACATT AGATCATAGC AGAACTATTT CTGTGAAGGT
5101 GTTTTAACCT TAAATTTCTG CAGGCATAAA AGAGTTTGTA GAAAATGTGT
5151 GGGTGTGGTT GACATTTTTT CTGAAGTAAT AATACAGAGG AAATTACCTT
5201 TCTTCTCAA AGTGTCTTA TTTATTTTGA ATCTTTTTTT TTGGTAGGTG
5251 GCCCAGGCAA ATAGTGTCT CATTTGGCCT ATGTCGTTAT GGTGGGAGGA
5301 TTGACTGCTG CTGGGGCTGG GCTCGCCAGT CTGGGGACA GTGTCAGCGT
5351 GAGTATCAAG CCTGGGGACT TCAGTTCCTT GGGAGGTGTG GCTTTCACC
5401 TTGTTTCATGG CTTACCCCA CATATCAGAG GGTTCATTAC TGAGCAAGGC
5451 TTGGCCTTGC AGGTCTGACT TGGGGATTTT CAGGTACAGT CCAGACTCCT
5501 TATTCTGCTT CTTTTCAGCT TTAGCCACCT GTATTACGGC CCAGCTTTGT
5551 CATTCACAGA GAGCCACCTT AAATGTTTCT TTTAGCATTT TTTCCCCCAA
5601 ATCTGCATCT CCTTCTGTT TTCTTACCAG GTTTATTNNN NNNNNNNNNN
5651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
5701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
5751 AGATGGGGAT AAGATAATGA GTCTAGACCG TATTTACTACT GGGGATAAGA
5801 TAATGAGTCT AGACCGTATT TACACAAAAT AAATCTGAA CCTTAGAGTA
5851 CTTATATAAT CCTCACCATA GCTGTGTGT AAAGTGGCCC ATTTGTAAAT
5901 CCTTTTTTGG ACTGGGGTTG TATTGACAGT GTTTTAAATG GACCACCCAG
5951 TATAATGAAA CAAAGCCACT GAAACAACAT TATTTGTAAG TTCTATAAGT

FIGURE 3B

6001 AACCAACCTC ATGTAATAAG TACCAAATCA GAAAGCTGAT TTTACCTTT
6051 TCTGTGACCA CAAATGGATA TTTTAATGGT AAAATTTAGA GCTACATCAA
6101 AAGAGTTTGA GAAATTTAGG AAATTTGTCC CCAGCATTTT ATCGCGATCT
6151 TAAAATTGTA TCTCACTCCT ACTGCAAAAA AATAGTCTTC AAATGATCAA
6201 GTACCTTTCC AGAGCACCCCT TAGAGTGCTT GGGGCGGGG TAGGGGGCAC
6251 TTCTGGTAAG ATGATGGGAA CTAAGTTGGG TTCTACATTG GGATATATAT
6301 TTTATTGCTA ATGAGGAGGA GGCTTAGAGG AAGAGAGAAG GGCAGTTACG
6351 AAGGCTAGAG CTGGCAATGG AGAAGCCTGC CTTAGAGATG GGTGCTAGT
6401 GTGAGGAGTC AGGCAAATTT AAGTTCAGGA AAGTTAGGAG TTCCCTCTGC
6451 TATTTTAATT TTTGAGGATG CTTGCAATGT CTTCTTTAAT TTTGTGAAAG
6501 AGGGACAGTG ACAGTCACAG ATTGACTCTA ATTGCACATA AAGACCACAA
6551 TCTCTGGTTG GGAATAGAAA GGTAAAGGAA ATGAATGTTT GCCTACCTGG
6601 TATGGAATTT GAGAACCAAC AGATTCTAAT AACCAAAATG TGAAGAAAGG
6651 ACCCTTCTGT TGGCCCAACA CACCTACACA TAACCCTCCT GAGTGAAAAA
6701 TGAGTAGTTC TATACCTGCA GTCTCCAGCT GTGCAAATAC TTCTGATACT
6751 ACAGAAGACT AAATTCACAC AGGCACCATT CTTCTTTTTT GATCATCTTC
6801 CCTTAAACAA ATATTGAATA GACTAACCAG TGAGTGTACA GCAGCTTTGC
6851 CTACTTCTTT TGTTTACTGG AAAGTGGAGT TACCACCATC TCCCTTTAAC
6901 AGAATGTAAT TGACCCCCCG TGCAAAGGGT CTAGCCAAGC AGCTCGCACA
6951 TAGCAGTTAG GCAAACATTC GTTTGCTTCA CCTTTTATGT TTATACTTCC
7001 AAAATCAAAG TAGTTCCAAG GTTTTCTATG TTACAGTGAA ATAAAATCCC
7051 TTTCAATTAA AAAGGCACAA ATGGTTCTTT ACTATTAACA TTGAAGTTGG
7101 TGAGGTTGTA AAAATTAGCT CAAAGGTGAA TGTTTCCTTC TGTGTATTTT
7151 ATTTTCCAG CATCTTAGAT GGCACAAATG TCTCTTGTCA GTTCAGAGTT
7201 CTGCCTGTCT TTGTTTTGAT ATAAGCAGGT AGAGGAATGT GGGGCTGAGA
7251 AGTAAGCTTG AAGGGGCAGA ACAAACCAAA AAGAGGCTGA TCAGATTGAA
7301 TGAAATATCT CTGAAAACCTC TTGATTATTT TAAAGAAAGT CTTTATGAAA
7351 TTAAGATTTT TGTCACTACG TTTGTTCAAG AAAATGCCTT GCTATTGTAT
7401 AACCAATCAA TCTAATATGA TTCCTTATAA AGATTCCAAA GAACCTCTAG
7451 CGAATTTAAT GTGAGAAATG TTTTTCCTT TTCGACCTTT AGATAATCAT
7501 GTAGTTCTTT CCCATAAGGA AGGGCTATTC TCCCTTCCTC ATCAGAGGTG
7551 CTCTGGTTCT CTCTTTTTCT GAATGATTCA CTTTGGAATT TTCCTTCAAA
7601 ACAGCATAGC AAAACAAAAA GAAACTATTC CCATTACTGC ATAGATCTTC
7651 CCAACTTATC CCATAGAAGG TGTGTTTGTA GGTAGGGAAA GGTGGTGGTA
7701 CCCTCATTAT ATTATTTAAC AGACCTTATG CCTTAGTGCA GTGACCTTT
7751 GGTGAGTGTT TATTCCGTTT GGTTGAGCAT TTGTGAGATG TTTGACTTAA
7801 TATTCATGTG AGTCAAATGT ACGTATCTGT ACAAACATG CTGCCCTTCA
7851 TTTTCACTTG CTATCTTCCT ATCCATGGTC TTGTTTGGAG AAACCGACTA
7901 ATGTTGCAGG ATGCTAAAGC TGGTAGACCT CTCCTTCTGG CTCACTATGT
7951 CTAAGCAGAG CCAGATATAG CTGGGAAACT TTATATCCTT CCCTCTAGGA
8001 CTCAGGAAGG AAGGATCAGA GATGCTACTC AAATGGGCAT AGAACCTGTC
8051 CTGCTGCTTC CTGCCTGTAC CACCAACAT TCTATCCCAA CATTCTGCCC
8101 TGCTAGGGAA AGCATGACCC GTTCCAGAAA TAGGCAGGTT GTGTTTTCAT
8151 AGTCTTTTGG TAGGTCATAC CCTTGGTTGN NNNNNNNNNN NNNNNNNNNN
8201 ATTCTTTGTT TTGTGTTCTT GACTCTTAAA CAGATCTCTA GCATATTGAA
8251 AATTCAACAT TTGATTTTCT AACTGTCATG GGCTTTACTT TTATTGACTA
8301 TTGATGTGGC TGTTTATTGT CAGGTGAAAA TTTTAAATA TGTTACACA
8351 CTGATGATTG CATATTTGCA GCACACAGCA TCTTAAACCA CTCAGAGGTT
8401 TGTACAAAAA TGTGTGTTTC TTGCTCTGTA ATTTTTTTGT CATTTTGATG
8451 GCATATTTTA ATTATGCTTT TATTTCTCTC CTTCTACCAA GTGGAGACCT
8501 CTGTAACAAA GATTTTTCAG GGTGTCATAT TTCATCTTTA AAAGCTGTGT
8551 AACTGTGGA AACAATTGTT AACCAAAAGC ACTAGATAAT TTAGGATAAC
8601 TGAGTTCAAG TTCTGACTTT TGTACCTGAA TAGGTGTCTA ACATTTCTCA
8651 GCTACAGTTT TCTTATTACA CAAGCATATT TCCAAGGTAT GTTGAAGCTC
8701 TAAACTGCAA CTGAAAACTT CCTTAATGTA GAAAACTAT ATAGGATCTA
8751 AATATTGTAT TTTTGTATGG TTGTCTTCT GTTTACTCGG AGATTTGACT
8801 GTATATGTGG CTTATGACAA TAGCATTTTT GTTAAAAGCA TTTTATAGAA
8851 GTGTGAAGAA AAATAAAAAA TACAACCAGT TCCAAGGTTT AACAAAACTA
8901 TTCCGTTTCT GAGTTCTTTG GCTGTCATTG AGCAACTTGT GGTTCCTGAA
8951 GGAAATTATG TGAATTAGGA TGGTTTTGTA TCATTTATCC TTAAGAACAG

FIGURE 3C

9001 GGAAAATTGA GATGTTTTCT TATGTTTTCTG CTGGAGATTT TGGAAAGATG
9051 TGAAACCTAC ACCTACAGAT TGACCTTGCT TAGTTAGCTC TGAACCTCCT
9101 GCTGCCTCTT CCACGTAAAG TGAAAATTTT GGATTCTTAT CGGCTTCAGA
9151 TAAACTTACA GGTTAGTGAA ACATAGGGAC TGAGATATAG TAATTCATTC
9201 TGAAGCTGTT TTGGAGTGGT CAAATAATTT TAGTTGGATA ATATATATTA
9251 CTGGCTAATG ATGTGTGGATA TTGGAAGTGA TGAAAAAATT ATTGAATTAT
9301 TTCTTTCTGC ATTTCAAATG AAAAGGCTAT TAGTTTGAGC AGAGAATTTT
9351 GATTTAGTAA ACAAATATT TAAATTTTCA GTTTCATTTT TTTCTCCTAT
9401 CTGGGTTTCA GATCTCAGTC TTATAAATGG AACATGATTT ATTTTGTGCTC
9451 CCTAAACTGG TTATTAACCT CCTGTCCATA ATCACAACAT TATATAGATT
9501 ATATATTTCT TTGATTATTT GGATTTTGAA TACTCTCTTT AAAATAATCA
9551 AGAGAAAATT AGAGCTGTGA GAATGTTAGA ATTTGTTTTG AAGGCCACAC
9601 ATAGTGTTCC CTCCACAGAG AGGTTATACT AGTAAATGCC TTTCTATTTG
9651 AGGTCAACAA CTATGACAAC TTCCATTGAA CATGAGTTAG TATTTTAAAC
9701 GTAAAGCAAT TTTTATACCT GTATGCACCC AAAAAGTAAC AGGGGCTCTC
9751 AAAAGGGGTG GGGATTGTAC TGTTTACATG TATATTGAAG ATTGCTAGCA
9801 GAATTCCTGG GCCAGCTTGG TGGAGCGGAG TACACTTCAT TGTCTTAGT
9851 GTAGTAGCTT CCTCCTCTAA TTTTGAGGTG AGAATGCAGA ATCTGTTTTT
9901 TGTTTGTGTT CTTTTAGGTA GGAATAAAAG CAAGGCAAGG AATAATTTTG
9951 ATTACTTGCA ACATTAAACT TGAATCCACA AATCCTTAGG AAGTGAAGTT
10001 TTTGATTGAA ATATTTTAA TGCCACTTTC CTTGAAAGGT TGTTTAAGAA
10051 CATCATGTAC CTTTGGGTAA CTCAAGTGG TCTTGGAATG CAGATTCCAA
10101 AGTAAGATCA CGGTTGAAGA ATCTTGACCT TTTCAAACAG GTAATTTGTT
10151 AGTATGTGTA GTCTTCAAAG TTAAGTTTCA GAGAAATTGC TTTGCTCTTT
10201 TATTCCTTTT CCATCAGAGA ACTGATCTTT ATGTAATACT ATTAAGATCT
10251 ACTAATTTCC TGAAATCCCT TCATAAGCTT AATCTGGCCA GGTCTTAACC
10301 TTTATGGATT AGAAATTTTA GTACTTCTTA AGCTAGAAGG CCAGGCCAAC
10351 TAAAGGGAAG CACTCTCCTC TCTGCCAGTT CAGCAACTAG ATCTGTCCTC
10401 AAATACCTGC CACAGGGATA TGCTGCTTGA AGTTGCCAC GCATGTACAC
10451 ACTGGGACCA AGAAGGCACT TCTGGTGCCA GAAACAACAC TGTGTTTGCT
10501 TTGTGGAAAT TTTTGATATG CTTTAAAAA TGTAGGTGTC TTCTCCCTCA
10551 CCTCCTGTGT GTAACCTCCA GCATTTCTTT TGTTTGCTTT TTATCTACAG
10601 AATTCATGTT CTTTGCATTT TGAGTTAGTT GAATCCACTG TATGCTTTCC
10651 AGATGATAAT TAGTGAAGCT CAATGATTCT ATGCAGTGTC TTTAGTGGG
10701 TAAGGGAAGA TATTCATCAC AGGGGTGGGC CTTATCACA GGGGAGATGG
10751 AAGGGCAAGG GAGAGGGATT CTGATGGCCT AACCTCAT ATTGCCCCC
10801 ACTGCCACAT GCAGACACTC TTGCCGCTTT CCCATTGATT TTGTGCAATA
10851 TTTTAAATTT TTCCACCAAT CTTTGGAAA TATTAATTTA TTTTGTAGGA
10901 GAAAATGTAT TCATTTCTTT AAATATCCCT CCTCAGAGCA ACAAGCATGA
10951 TTAGTTTTTG GTATACTTTA AAAAATATTT TACCTACTTA TGGGTAAATT
11001 GCAATAGATC TCTCCCCTAT CACCCACTTG TTTTGTACAA ATGAAAGCAT
11051 ACTATATACA CTGCTTTGTA TGCTGCTGCT TTTTCTTAAC TGTACATGTT
11101 GAAAGGTTTT ATTTATAGAC CTCTTACNN NNNNNNNNNN NNNNNNNNNN
11151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNC CTCCTTACTT TTTTATGCAC
11451 TCNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
11551 AAAAAACTTT GAACATATGT TAAAGATGTT GTTTTGCATG TTCTTAGTGT
11601 TTCTGCAAAA TAAATTTTTA TATGTGGTCA AATGGCAGAT ACATTTGTAA
11651 TTTTATCAA TTGCCAATG ACTTCTTACT CAGTAGAGAA GATAGTTTAA
11701 GGGGAAAGAC TGAATGGCGA TGCTGACCCA AAGGCTCCAA CAATCCATA
11751 TCCAGAGTCT GATCTTTCCT TGATTTTAGG ATTCTTTGAT CCCTTTTCTT
11801 TCCCAAGAAA TCCCTCTGAC AACTCAGTGA ATGTCCATCT GCTCCCATCA
11851 TCTGTTTCCC ATCAGACCAG AGGCAATGGG CTGAAGCTAG GAGAATGGAG
11901 TGAGATGTGT CCATTTGCCA GGGTCTCCCA GTGGCTTCCT GCCTATCATT
11951 TACTTGTAAG AAAGAGCCAC GCATTCCTTT AGGAATTGCT TAATTCATTG

FIGURE 3D

15001 ATATTGATGG TGCATCCCTG GGAACATGCC AGGGCAAATT GGGGTGCAAA
15051 ATACACCAGT TATTTAAAAA TTGGTATGTT ATAAGGTAAA GAATTCATTA
15101 AGTAATATCA AATACAAATA AACTTTTTAT TTTGATTCAC TAAAACTTCT
15151 TTTTAAGTTT TCTGATTTTA TTACTTAATT ACTACTGATA CATAATTAAA
15201 GAATTATGGC CATAATAGAA TTCCTAATAA AATTTCTAAT AAAGCCAGAA
15251 TGAAGGAGTA TATTACAGGC CAGACATGAT AAAGCATTAT GATGTGTGGT
15301 AAAATAGTGA CATCTATTTT TTCATTCTGT ATTATTTTAT AAATTTTCTG
15351 GAGAATTTCA GTTTAAACAG CCTGCTGAAA TACTGTTAAA TCAACCTGTT
15401 ATTCTTAAC TGTATGGGAG GAAACAGATA TGAATAATAA AAATGATTTC
15451 TTAGCTTTAG AATATAGTTG TTGCTTTGGA GAACAAACCG TTTTATTCCA
15501 ATTATTTTTT ATTAGGAGAC TTCATTTTCT GCCATACATT AGCTTTGGTA
15551 GATACTAGAT GCCAGGGGAG TGCAAATTTG AGAATAAGGA TTTGGCATGG
15601 GTTATTTGCA TGTGAGAGT CAAGATTTAA CTAATTTTAA AAACCAACA
15651 CTTCAATTGA TCAATATCTT TTTAACCATT CTGTAGATTA ATAATATAAA
15701 TTCTCCAGAG CTGACATTAC TTTGCTATAA CATCATCAGA TCACAAGATT
15751 AGGGTTGCCT TTTGTAGATG TTATTCACCT ACTCTGAAAT GTTAGGAAAT
15801 ATGTCATCAC AGTTTAAATT TGTAAGTAATA TATACAAAAG GAAAAACACAA
15851 CTAGGAATTT TGGATTTATG CTTACTTTGC CAAAAACCAT GTTGATTTTC
15901 AAAAACCTTT AGCCNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
15951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
16201 NNNNNNCTAA CCTTATTTTC GTAAATCAAA GTTCCTAAAT TCAGTTTCTA
16251 AGGAAAGCCC CTAAGTGGTC AAAGGTGTGT GTTGCTGAAT TTCAGAAACA
16301 AACTCCATGG ATGGACTTTC CAGACATAAA CTTCCCACCA AAATATTGTT
16351 CCAAAGTGTT TAGTGCCTCC TATTTTATTT TAGTGTTAAG ATTTTGTAGG
16401 TACTTGGTAA TTATCAGCAG AATATTTACA TACCAACAAA TAGCAAAGCC
16451 ATTGATAATT AATAGAAAAA CAAAATCATA GCTTATGTTT AGTTGTATTT
16501 TTTAGTGTAT TTCAGTGTTC AGAGTTGATT TTATATTGCA TATACTAAT
16551 GTGTAATAG TTTCTACTGG ATAGATTATT TCAAGTTCAC ATGATTATAG
16601 AAGTATTTTA TGAAGTTTGA CATAGATAAT GGTGGTTTCA GGGTCCCTTG
16651 TCTCTGGGT TGAGTTTTC CATCATTGAA GAATTAAAAG ATTTGTGCTT
16701 GGTGTCTATG TAGGCCAAG AATTAAGACA TTCTGTGTA CAGTTTCATT
16751 TTCTAACTAA GGCAAAAATG ATTTTGAATA CAATTACTTT TTAGGATAAA
16801 AGTATAAAAT TATGAAGAAA TAATGTGTAG GTTTGCTAAA TGTGTGTGTT
16851 TTAAATCTTG TGTGAGGTC TGATGAATTT TTTTATATCT TTAATAGTTC
16901 TAAAGTAGTG TACTGAAAGT TAGGATCATC CATGTTGCTA CTTAACTTGT
16951 TGTCATAGG GTCTGTTGTC CTGGATGTTG GTGTTATAAA TGTACAGAGT
17001 TAGGTAGTTT TCTGTGAAGA GTTTGCAGGC TAATATCACT GTTTTGTGACA
17051 ATGAAAAATA TAGCATGAAA ATTAAGGTTG GGGTATGGAG AACTTTCTAG
17101 AGCTATTGCT TTTCTAGCT GATGATTAAG GTTGAGAGGC AGAAGTACAT
17151 TGTGTACAGG AGGACCTTTC CCTTTTATGC ATGCACCTGG CATTTATCAC
17201 CTTTAACAAA GTGTGTGTGT CATGCTGTGC TGCTTGCTTA AGGGGCTGTA
17251 TGCCTCCAGT CTGAGTCACA TGGTAACTGC ATCAGCAGTC TTAGCCTGTA
17301 GCATTTTATT ATTTCTTTTC AAAGTTTACA CTTGGCCTAA TACTTAGACA
17351 TTTTATAATT CTTTACAGTA AATGAACTA TACATGAGAA GATGGGCATA
17401 CCTTTGGATT AAAAAAATAA AAGGCTCAGT TCTTTAAAGT TTCTTATCCT
17451 TGATTTTCTT AACACGGTCC AAAGTTCAGG ACTGGCTCCA AACCATAAAA
17501 CCTGTGTTTA GCAAGCAAGA AACATAATCC CCAGATAGTT TAGTTTCTCT
17551 GGTTTATGAG TCACAATTTT ATAAAATCAT CAGAGTGCTT ATTAATTCCA
17601 ACCACGTATA GTAAAGAACC TTCAGATGAA CTGAAGCAAG GGTTCCTTAGG
17651 CAAGTTGCCG GAGAGAGTTC TAGAATTCTA AACTACCTGA GTAGCTTTGC
17701 TGAATGTTG CTTGTATTTG CTACTGTGGC CATTTTATGA TGGCCATAGA
17751 GCAACAGATT ATCAAGAGAA AATGAGACAG ATTTTCTGTT ATTATGTGCT
17801 ATGAATGAAT CCTATTTTAG TGAATGTTTT AATGGGGTTT ATACCGCAAA
17851 AAAAAAAAT TGATGTAAAG GCATTTATTT CTGGCAACTT TCATAAAAAT
17901 TGTTGTGATG GTTGCATATA AAAATTTTCT TATCCTTCAA TAGAGGATAG
17951 TTCCCAAGAA CTTCTAGAAA GTAATCTATT CCAGATTTAA CATTGCTTTG

FIGURE 3F

18001	ACATAAAATG	CAGTTTTGTG	TAGTTTTTAA	ATGCAAATTA	AAAAATATAG
18051	GACATTGGCT	AAAAATTTAT	CTTGAAGTCG	GGTATATATT	GATACCATAA
18101	AACTTACTAG	ATCTATGTAT	TTCAAGGCTA	ATTTATGCCA	AGTAGGAAAA
18151	ATATGACCCA	ACCTTAAGAT	ATTACAAGGA	TAAAATAGAC	TATACAAAAC
18201	TGTTTGCTA	TTTGGTACTA	ATACAACCTAG	TTAGAACATA	ATGATGTTTG
18251	CTATTCTTTA	TTAAGTTGTT	TTACCTTTGC	TTACAATAAT	TTAAAGTATT
18301	TTTCCTGATA	AATTTGATGA	CTCAAAATTG	GCAATTAAAG	AATATTTAAAG
18351	AAACGGTATC	CTTTTATATT	TTTTCTGTCT	CATATATAAC	CATAGTCATA
18401	ACTTGTGTGA	TCCAGAATGT	AATTTGCTAT	TTACACTTTG	ATTTTCAGCTG
18451	TTTGCTTAGA	TTGTACCTGA	TGTATTTTAT	TATTCTATTT	AAGGAATGTG
18501	TCAACATCAA	GATATGGTGA	GTTCTTTTCA	AAATAACAGT	AGAAACCTGA
18551	CCAATATGAA	AAAAAAAAGT	CTAGCAAGCA	AATGTAATTT	GTGTCTTTTAA
18601	AAATACATAG	CAATCATTCT	GGATCAATAG	TTAAATTATT	GCTTCAATTA
18651	AATCAAATTG	GACTTAGAAT	TTTTTTCTTC	TTATATTACC	CAAAGGAAGG
18701	CCCCATTAC	CNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNAA
18751	TTGTAAATTA	CAGTGGATAT	TTAATCCTTT	AAAGGCATTA	ATTTAGCAGA
18801	GAAGAATAAA	ATTATCCCTT	TTCTTACCTC	TAAAATCTCT	AGGTTGATCA
18851	AACACTGACC	ATTATTAGTA	CCATTTCAAG	TTTCTTCCCT	TTACTTTTCAT
18901	CAAACCTGGT	TATTATATGTA	TGTTCAAGTG	AAATGGCTGT	GCTTTCATGG
18951	TAATTCTTGT	TGCTATTGAC	AACCAAAGCA	GCCATGCAAG	AAGAAAATGC
19001	TGTGGAAGGG	AAGAAAAAAA	TTATATTTCC	TCCCCAAAGT	TGGAGAGAGA
19051	AGGGAACATA	CAGTATGTAA	GAAACAGGTA	AGTAAAAATA	TATCAATTTT
19101	AAAACATATTA	GCCTTTCTTA	CTAATTGATC	AAAAGTTTAA	ATTTTTTTCAG
19151	ATGTGTTTTT	CAACTCCAAT	TTAAATAAAA	GGATACTGTC	TCTAGGAATC
19201	AGAAATTAAT	ATTCTGGAAA	TGAAAAATTG	GATTTGAAAA	TACAGCATCA
19251	CAAAGGTCT	GAAATATTTA	AATTTAGAAT	TTGGACTATA	GAAGAATAGC
19301	ATAACTTCAA	TTATTGGTTA	ATATTTTTGT	TATGAAATGT	TTTTTTTATAA
19351	CAAAATGGTG	ACTAAAATAT	TACTATTTTA	AACATGTCCT	AGATTTTTTT
19401	TTGTTTCAGA	AAAGCACTGA	AAGTTGAATA	TGTGTAAGTC	TCCGGGAATG
19451	TAACAAGTTG	ATAAATACCC	AAGTCCAGCC	TCCTTACAGA	GAAAAGATCT
19501	GGAAATTTCT	TTTTTGGACA	TTTGTTTTGC	AGCTTTCTAC	GTCTTAAGGC
19551	AGAGAATAGC	CAGGATAAGG	TGCCAGCTCA	AAGGTTAGAT	GAACATATTT
19601	CTTGAAATAA	TTTTGGCTAA	TCTATGTCTT	GAAAGGCATA	CCTTCTAAAT
19651	AATTTTACAA	AGCTGTAAAC	AAAACATTAG	TTGTGTTTTT	GAATTGCTTC
19701	TTTTTAGGAA	AACTATATTT	CTTAGAGATG	TGCTTATTCT	ATACATAATT
19751	ATAGTAAGTT	AATTTTAATT	CCATTATTAC	ATTAAACTTT	TCCGTTTCAG
19801	TTGATTATTC	CTTCTTCTG	TTTTATGAAT	CTAATAAATT	GACCTCCATT
19851	CTAAGCTAAA	GGACAGTTTA	TGTTTTTAAT	ACTTAAGGAA	GCAAATATAA
19901	AAACAAAGTC	CACCAAATGA	AATTACTAAC	ACCAGCCTAT	CATTAACTTG
19951	AGGGAGTTGT	ATTTCATATT	CATTAATTCT	CCATGGAACA	ATTCAGGTAA
20001	GAAATATTTT	TATTGTATGA	AATATGTTAT	CAGTTATAAT	AGCACTTACG
20051	GGCATTTATG	CTCTGTTTT	AGGTACATAA	AGGGTTCCCT	GTTTAAGATA
20101	TTTTTGGCAG	TAAATAATGT	CACTTATCAC	CCTATGACAC	TTTAGTGGAA
20151	AACGTTGGTG	AAATATGTGG	AATTGTAATG	TTTAATGGAA	TTGATTCTAA
20201	GAAGACAATG	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20501	NNNNNNNNNN	NNGAGAATGT	TCTTTAAACT	GATTGAAGAA	ACTATCACAT
20551	GTCAAGAAAA	ATGTTTTTAA	GGCAGNNNNN	NNNNNNNNNN	NNNNNNNNNGG
20601	AACAAAATTG	ATAGTACTAG	AAATAGAAGT	TCAGAAATTT	CTTTGTTTCAG
20651	GGAGACTTAA	AGCATATGTA	TTTTAAAGTT	ACTAGCAGTT	ATAGGATTGA
20701	CTAGTAGAGC	TATGGCTTAC	ATTAGGGAGG	CAATGCCAAG	GAAAGAATAG
20751	AATGTGTGGT	TGGCCACCAA	CATNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
20851	NNNNNNNNNN	NNCTAACTTT	GCAAGATTCT	TACTGGTTAT	AAGGAGGTGG
20901	CTTCCACAGT	TCTTGACAGA	TGTTTGCTAT	TATTAGTGTG	TTCTCAATAT
20951	ATACAATACA	AATGGGAAC	TCTGAGCCGA	GTTTTACTAG	GATCCATCCT

FIGURE 3G

21001	AGGACAGATG	GTACAGCACA	TTTTCAAATG	GTTTTGTTTA	CCATAATCAT
21051	CTTTTGGAAA	TAATCAATTG	GAAGTAGAAC	AATTCTTCAG	TTATTCATT
21101	CTAAAATCAA	AACCTTCATG	GGATAGTTTT	CTGTGCTTCT	GAACCGTTTT
21151	TCCCATTCT	CTAATAATAT	CCATCCATAA	ACCTCCGAGT	GGAACAGTTT
21201	TGGTTGTCTA	ACAGTGTTTG	TGCTTGGGAA	ATGAATTGAA	GGGAGATGGA
21251	ATTGAATTGT	TGAATGTGAG	CATTTAGAGT	TCCTGTAATT	TATCCGTNNN
21301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
21351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTTG
21401	TAAGATGATT	GGCTCTTATT	CCTTCTATGA	TTCTTAAATA	GGAAAAAGTT
21451	AGGGATAAAG	ATTTGAGGGA	GTTTCAGGGAA	AGAATCATTT	CCTGCTGAAG
21501	AGGATCAAGG	AAGACTTCAT	GAACCTCAATG	GTATTCAGTT	GATACTATAT
21551	ATATATATAT	TATCAGTATA	TCTAGTATAT	AGTATCAGTA	TTGAAAGCCC
21601	ACAGAGGAAG	GCAATACTGG	GTAAGAGGCA	TGTTTTAGTA	TAGGATTCTG
21651	TGAGAGCATA	TCTTAAGGGG	CAGTAGCCCA	GACCAGCAGT	GATGGAGTGG
21701	TGATGGCCCC	GCTGAATCCC	GAGGGATAAA	TCAGTCAAGT	GAAGAGTATC
21751	CTGGGCACAC	AGAAAAATGC	ATTTAAAGCT	CAGTAGCCAG	AGGGAGGAGC
21801	ACATTCCGAG	AACTGTTAAG	AATCTCAACC	CAGCATATGT	GGGGTATATG
21851	TTTGAAGGGC	ATCTGATGAG	AGACGCAGTG	GGAGAAGTGG	GAAAGGACTC
21901	CTGGAAGGCT	TTTGATATCA	TATTAAATAC	ATTTGCCTTA	ATCACAAAGT
21951	TGTAGAGGAA	CACTGTAAAG	ATTTTAAGCA	GAGAAATTAA	TATTTTAGAG
22001	GATAGCTGGT	GGTAATGGAT	CAGATCTAGC	ACTCAGGTGA	ATTTAGTTTT
22051	GCTTGGAGTG	TTTGTAGTTG	TCAGTGTCTC	ACAGGAGACA	CGGATATAAG
22101	GGTTGGTTCA	AAAATCGGTA	GGTCTGCATT	GCTGCGAGGA	GTCTATCAGC
22151	TGGGGCCTCT	TAAGTAGCTG	GCCCATTG	AAGAAGTATG	TGCCTCATTT
22201	CCCTGTGGAG	CTCACTTCCT	TTAGTGCAAA	TGCCTGGGAC	CTGTAGGAAG
22251	TCAACCTGGT	GAGAAATTAG	GCTTCATTTT	AAGTAGTGGT	GGTGGGAACA
22301	AAGAGAAGGA	GAGGGATTGA	AAGATACTGA	AAAGAAAGGA	TGGAGAGGCA
22351	CACAGTGTTA	GGGCAGTGGC	GGGGGGGCAC	ATGGGCTTGG	CAGACAGACT
22401	TGNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
22551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNCAGTATT	TGTAATGCTG
22601	GTTGTGAAAG	GTGAAGAAGA	TGTAATCAAG	ATTACTCCCA	AGTCTCTAGG
22651	ACATCATTTG	GTGAGCTAGA	GAACACAGGA	GAAGGTGCAG	ATAATGATTT
22701	CAATTTTGGA	TATGTTTCAGT	TTGAAGCGCT	TGTGAGACTT	TGAAGTAGAG
22751	AAACTTGATA	TGTGCTTGGA	TTGCAGGGTG	AGATCTGAAC	AGAACACAGG
22801	CTATGATTTT	ATTTCTTTCC	ACTATTCTAC	TCAAACCTTC	CTTCCTTTTC
22851	CTTCGTCAAC	TTCACTCAAC	ATTGATTATT	GCCACAATA	TCTCCACGGA
22901	GGAACAGCTT	TAAACAGTAG	AAAAAGAATG	TGGGATAGGT	AAAAATCTGT
22951	GTTCCACATC	TGCTAAATGT	TATCTAATAG	TTGTAAGTTC	TTGAAAAAAA
23001	ATCTTTCCAG	TTTACCGTTT	TGGCAAAGCA	TTGTAAGCAA	CTAATAATTC
23051	AACATTTGTT	TATATCAAGG	GCTGAAAAAA	AGTCATCCTC	TACAAACATA
23101	TTTTCTTTTT	TTCCCTCTTT	TGTTTGCCTT	TTTTTGTTTT	ACATCACCAC
23151	CACTCCTAAC	TCTAAGAAAA	TATTTGACTA	AAAGTGAATC	ATTGTTAGTA
23201	GTGAATTCGT	ACNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
23501	NNNNNNNNNN	NNNAGCACAT	TTATTTTTTA	AGTTTATATT	CTGTCCTAAT
23551	ACAATGTATT	AAAAATGAGC	CCTGCCTCAA	GTCTAGCCT	AAATGCCACT
23601	TTCTCCAGTC	TGCTTTCCTG	ATTTTCACAG	CAGGAAGTCT	TCTGTACTTC
23651	CTCTACATAT	AACACTTGCA	TGAAGCATAT	CTCACATTGC	CCTACATTGT
23701	GGTTATTTAT	GGATCTATAT	TATTTGTTCT	GCTAGACTAT	TAGTTTCATG
23751	AAGGTGGAGG	CAGTGTCTTA	TACATCTTTA	CGCCAGTATA	ACAGCTTCTG
23801	CAATGCCTCG	TCCAGTTCAG	TTCAGTACAC	TTTTGAAGGT	GTAAGAGCTA
23851	GTCATTTCTA	TTTATTAATA	AAAGGGATTT	AAAAAAAAGA	TGGACAAGAT
23901	GTAATCTTAA	TAAACATATT	GTGGTTTTCA	GGAAACAGTT	TAATGAGAAA
23951	ATGAATATAT	TTGTCTCCCT	ACCTTATGAC	CTTATTACAT	ATCATAGATC

FIGURE 3H

24001	TTCACCTCTTG	CTTTAGATTC	TAAACAGAAA	TCAATTTATG	TGCTTGAAAT
24051	CACATAAAGG	TAATCTGATT	GTGTCATCTA	CTGCTTACAG	TCCATTGGCT
24101	GTTCAACAATT	ATGGGTAGAA	TCTTGATTAT	TTGAGTAGAA	GCCTTTTCAG
24151	GCTGACATTG	CCTTATCAGT	GGAGGACTGT	TTCTTGTTGT	AGGCCCAGTC
24201	GCAGTGACG	GCCCTTGGGT	TTCCAGACTT	CTGCTGCTTC	ATGCCTGTTG
24251	GCTTTTCTTA	TGCTGCTCAG	TCTGAGTCAA	AGGCCCTTCA	CCCATTTCCCA
24301	TGGTGAATTT	CTACTTATCC	TTTAAAATTC	AGCTCACATT	TCCTCTTGAA
24351	AGTTTTTCCT	GGTATCTTTC	CTATTCCTGC	CTCCCTGCAG	AGAAATGCCT
24401	TCTTCTGTAT	TCTTTTAAAC	CCTTGACAC	CTGTCATGTC	TATCTTTGTC
24451	AGGAGACTGT	ACACTACAGA	GCAAGTACTG	TGTATTTAAA	GAGCTCAAAG
24501	TCTAGTGAAG	GAGCTAGATA	AGAAAAACAA	CTCTGAAAAT	ATGGTATAAG
24551	ATATATATAT	TTAAAAGTAA	ACCTGTATAT	ACATATAATT	TATGATAGAA
24601	GTATGCACAG	AGGCTTATGA	AAGCACTGAA	GAGGGTATGA	ACTCAGCATG
24651	AGGCGTGAAG	ATCTTGGGGG	TGATATAATG	GTCAAACCTGA	CAGGTGAAGC
24701	CTGTCTAGAT	ATTAGTGTAG	CAGACAAGAG	GGGAATGGC	ATTCCATGTG
24751	AAAGTGTTGA	GGTACTCGAG	AGTGTATTTT	TAAGAAGTGC	AATTAAGTGC
24801	TATATTTGTG	AATGTGATTG	GAAATGAGGC	CAATGGGATA	GGCAAGGGTC
24851	ATATCATGAA	ATATGGTACT	GAATGCCATG	CTGAGTGTTC	GAAATAGTAT
24901	AATGATCTAC	ATGAACATGA	TGAGGAGCCA	GTGAATGAGT	ATAAGGAGCA
24951	GAATGGCATG	CTGAAATCAT	GGGTTAGGGA	GGTCCCTCTA	ACAATAGTTC
25001	AGGCCTGGAT	TGAAGTCCAT	GATGTTGGAC	ACAGAAAGAC	TGTNNNNNNNN
25051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25101	NNNNNNNNNA	AGGTTCTTCA	ACAGATAAAT	TTGGAATAAT	TATCATTTTC
25151	TTTAGAAAAC	AAATAAGCAA	ACTAAAAACA	CCTGAAGGTC	AAAATGACAA
25201	ATCTCTGACA	TCATATTAGT	CGAGGCCCAG	TAACAAAATT	GNNNNNNNNNN
25251	NNNNNNNNNN	NNNNNTATAC	TTCAACTCAT	GTATCAGTGA	CTCTTTTAAA
25301	CATAGAGATT	TTGGTTGCTA	AAAAAGGTGA	TGATGGTTAC	ATTAAAATTT
25351	TCTGGCCTTT	TGTGATGATT	CTTAGCAAAA	CCTGCTCAAA	ATTACAGTAT
25401	CAGATGTTTT	AAAAATGAT	AATTTTCAAC	TGAAAGAAAT	ACTGTAATGT
25451	ATTTTCATCAT	ATTCTATGAA	TTCTTACATT	ATGAAAGATA	TCTTTTATGT
25501	TTCAGATATC	TATTATATTT	CCTTTTGTAA	AGAATTTTTT	CTAGCACTAC
25551	ATCTTTTCCA	AACCTTTTTG	ACTTTCCTAA	GCCTGTGTAA	TTAATCACTG
25601	CCTGTTCTGT	GTCTTAACA	TGCATCTGTT	ATCAGGACAT	CTCTGCTTAC
25651	TTCTGTTTCT	CCTTACTAGA	CTTACCTGCT	GGAGGATGAG	AACTTGCTCT
25701	CCTATTCATT	TTTATATCCC	CAATTTTAA	TATAGTGTCT	TAGACACTGG
25751	GGCGTTTCCT	CCTGTGCATA	CTTATAATCC	TCNNNNNNNN	NNNNNNNNNN
25801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
25951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNCCTT	TCTCTAAATT
26051	ACATTGAAAA	GTTAACAAC	ACTCACAAGT	TAAATAATAG	TTGTCTGTGT
26101	ATTCATGTTA	TTGTACTCCT	TTTATATAT	TTCTTCCATG	NNNNNNNNNN
26151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
26951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 3I

27001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
27351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTAC	TCTACTNNNN	NNNNNNNNNN
27401	NNNNNNNNNN	TTCACATTTC	CAAATAAATA	GTAACACTTT	TTAATGTGTT
27451	CTTAACGTTT	TATTTGGCAT	TAATCTAAAT	TCCCCTCTAG	CACAATGAAA
27501	ACAGAAAGAG	AAAGTTAAAA	TTTCAAGTAA	ACTGAAAACA	ACAATAGTGC
27551	TCAGAGGATT	TTTTTTTAAAG	TGAAAAGGGA	TAGTGCTTAA	TTATGACAAA
27601	TAAAAGCTAA	CTTGAGATGC	ACATATACAG	ATGCAGCCAC	TTATTTTGGC
27651	GGGGGACACT	TCAGGAATTA	AAATTTAAAT	AGCGAGAGAT	CAAATAGATA
27701	CTTGGTAAAT	GTGTCTGAAT	TGGATGTTCC	CAGACACAAA	AATAAAATGA
27751	GTTATTGACA	GCTCTTGGGA	GACAACATTA	TAAAGACTAG	ACACGTTATT
27801	TATTTTAACT	CTATGTTCTA	AATTACCATT	GAGTAATTGA	CATTTCGTATT
27851	TGACTATGGT	TTGTGGTTAA	GTTCTTAATT	GCAATAATGT	TAAATAAAAT
27901	GTGAAGCCCA	AAGCAAACAA	CAACAAAAAT	TATAGCAATA	CTTCAACAGA
27951	GGTAATAATA	ATATGCTGCA	TCAATGGTTC	AGAATCCAGC	ATCTACATAA
28001	AACAAGCAAC	AGGGTAATGA	AATTATTTTC	TTTTCAAATA	TTCTGGCAGA
28051	GCTACTTTAG	TTTTCTTAAG	TTATAGATTG	TGGTCTTAAC	TGCAACTTTT
28101	CGCTCCTTTT	AAGAAGTATT	TAAGTTATTT	AAATGTTACT	TAAATACTTT
28151	TATGTTTTTA	ATCATTATTA	ACATTCTCTA	CCCCTCTCAT	CCTTTCCTGC
28201	TTAGTATTTT	GTTATAATCT	CACTCTCCCC	ACTTCCAAAT	GCACTCAAAA
28251	ATGCTGGACT	TTCTGGTCTT	TTCTGACCA	CCAGAAGAAG	TAGTGGATTG
28301	AGCATGGAAC	TGGGATAAGA	CATTTTTCCN	NNNNNNNNNN	NNNNNNNNNN
28351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
28401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
28451	NNNNNNNNNN	TGAGTTCTGT	ATTCATGAGG	GCATTTAATG	TGTCTTATAG
28501	TGATAACAAT	CAGAGGCATT	ATTATTCAGT	TTTTACTGCA	GCAGGAGTTT
28551	AGATTTGACC	ATCAGATAAT	TGACACTATA	GTACAGGGTA	TTAGGAAAGC
28601	TGGAAAGATG	CTTTCCCTCG	GAGATCTTGG	ACAGTAGGAT	TCTTCTAGGT
28651	TTTGTCTGTC	TCATGATATG	CAATGGCTCA	GGGCACTTTT	CAGAGGACCA
28701	CTGTACAATC	TCCCTCCATT	CCACCCAGGT	CCTATTAATA	TAGTAGTGAG
28751	TTGTTTCATA	TTGCCTTCAG	TGACTTTCCC	TTTTCCAAGG	CCAATTACCA
28801	TTTGAAAAAG	TCATTCCCTG	TCATATTTTC	TTGTTCTGCT	CAAATGAATT
28851	TGTCCATATC	TGAATTCTGT	GAAGCTTGTT	GGGTGTAAAA	ACAGCTTTTC
28901	AAAGCTTCC	AGTTTCATAT	CTATTTGTTC	TTCTGCCCTA	CCCTTGCAATG
28951	TTTCTCTGTC	CCCTTTTCTT	CTGTGAGCAT	AACCTGGAGG	ACAAGGTTTTT
29001	TTGTTCTGTC	TTTAGTGGTG	CCATGTCTGC	ATAATAACAT	GATGTAGATT
29051	GAAAAAATTA	CAAATGATTC	TTGGAATTCT	AAAGATAATC	TTATTTCTAT
29101	TGAGAAAAATC	CTTCTCAAGT	TACTAACTAC	CATTGAGATT	GGATTGGCTT
29151	TTGCCTTATT	ACTTTTCAGA	GCCTCCATCT	GCTTGGGTAT	CTCAACATAT
29201	CCTTAGTTTT	CAAAATGTTG	CACTTTACTC	CCAGCATGAT	TACCTTACAT
29251	AAGAAACATT	ATAGACTGA	TGTGGGAGTT	TACTTTTCTC	ATAACTTATT
29301	TGATAATTCA	CTGCTTATGT	TAGAGTTAGA	AACTATTGTC	CAACTCTCAG
29351	AGACCCAGTT	ACATCACTTA	AGATGGATAN	NNNNNNNNNN	NNNNNNNNNN
29401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
29551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNGGAT
29601	GGATTTTTTAA	GACTAAAAAT	TTAGATTGCA	ATCAAACAGA	AGAGGCTTGG
29651	ACATGTGACA	TTAAAGAGCT	ATGTTTGTTT	TGCCAGTTGA	AACTTGTTTC
29701	TTTTTCTAGT	TAAAACAATG	ATTTAGAGGT	TATTTTGAGG	GCACTTTGAA
29751	GATTATGCTA	CAGGAATGCT	AGAGAGCAAA	TTTTGAGAGT	GATTGCCCAT
29801	TTGGACTTAA	TTCTGGCAAC	TGATTTTGGG	GTAAAATGTC	TATCATTCGT
29851	TGATTATCTG	TGATTTTAC	CTGGACTTTA	CTTAAGCTTT	ATTAAGTTGC
29901	TAAACCATAT	TTGGATGCTA	GTGATAGCAG	ACCATCAAAT	ACGGCCCAAA
29951	CTTCTTGTTT	TGATCCACAC	GAAGGTCAGA	GAAGCAATGC	TGCCTTTTCT

FIGURE 3J

30001	GATAGCCAGT	AGCACCAGCA	GGCACGTTGT	TTACTCCAAA	CAAGAATTTT
30051	AATATTTTTG	AAGACCACTG	AAAATGGATC	ATTTATACTT	TTTTATTTTT
30101	TTGATAAGGA	AGGGATGACC	TACTATTAC	AGAGTAATGC	AGTTTGCTGA
30151	AAAGGTTGGT	TTTTGCTGAC	CTCTGAGAGC	TCACATTACA	GTGGAGTGTG
30201	TTATTGGAAG	GTGAGCCAGT	TTATACAGAG	GTGGGAATT	ATTTTTCTCT
30251	AGTTTTGAAA	TGGTTATGCA	CTTCTAATC	TAGTTATTTA	GATGTAGAAA
30301	TAAAGTTTTT	TTTTTACATT	CCCCTGAGTA	TATGGTATTG	TAGGTATAAA
30351	ATAAATTTGA	TGAGTTTTAT	TTCTGTACTA	GGATCTACTC	ATAACTCTTC
30401	TATCCTAAAT	TTGTATCAAA	AGGAAACCTT	TGCTGTCTTG	ATAATAAACA
30451	CAGACTAAGT	CCAGATTCCA	CAGTCTAGTG	ATCAAGGAAA	TTCAGGAATT
30501	GTATTTAGCT	ACAAGTAACG	TGACACAAAG	AACAGTGCCC	TAAATTGCTA
30551	GGATGGTGAT	TTAGGGTTAA	TATTATGACT	TCTTGCTCTA	CCCTCTTTCC
30601	ATTCTCAAGA	TCGCCTCATG	GTCATAAAGA	GGCCACTGTG	GTTGAGTCAT
30651	GACATGCACG	TTCTAGGCGA	GAACACAGAA	CAAGCCGTGC	TCTTCAGCCC
30701	CCTTCTTACA	CAGCATTCCA	AAGCCCCACC	CCATCACTTC	TGCTTTCATC
30751	CCATTTAGCC	AGAACTTAGT	CATTGGCTG	CCCATATCTG	CTAAGGAGAA
30801	TAGGGAACAT	AGTTTTCAT	TACTAACCCA	TCCCCCACTC	NNNNNNNNNN
30851	NNNNNNNNNN	NNCCATTCTA	TATTAAAGCA	GAAGGGAAAG	AGATATTGGT
30901	AAGAATCCAG	CTGGCCTTTT	GTGATCTGTG	TCAGCCTTTC	TTTTGATCTC
30951	ATCTGCTGTT	TAAAGCACTT	TACACTGTAG	CCCCACGAGA	ACACTTTGCA
31001	CTACTAAGA	AGCAGTCCCC	TTTGCTGCGC	CCCCCCCCCA	CCACTTTGCT
31051	TATATTCTGA	AAGTCTTTTG	TTTCCTATTC	CACTGCTCTT	ACCTCTAACA
31101	CACTGCCTCT	AACACACCAA	CCTGCAGTTG	TAGTTATTAC	ACACCTCCT
31151	TGGTCTTTTC	ATCTCTCTAT	CACAGCCCTT	GTTGTGGTTT	AGCCAATATA
31201	TTTTAGTTCC	ACAGCTAAAT	TTTCATACCC	TCTATGACTC	TCTAATCCCC
31251	TGCCACACTT	GCCTACTATA	ATACATTATA	TATATAACAA	ATGTTTGATA
31301	CGTATTTATT	GAATTCCATT	CCAGAACTAA	TGCCAGCAAG	ATAACTTTGT
31351	GCTATATAGG	AGAATATCTT	TTTGTGCAAC	AGTTTCCAAA	GGGTTTCTT
31401	TTTCTAAGAA	GAAAGAAATT	GATTGTATCA	ACTTTATGAG	TATCCTACCG
31451	CATTTAATAG	CCATTGGCTA	ATCTAAGGGT	TCCTGGTTAC	TTCATGAAT
31501	AGCCTATCAG	ATGGAAGTGC	AAACAACAGT	TTGTTTTGAA	ATAGGACTCC
31551	CTAAACATGG	AAGAAACATT	AACAGTGTTG	GCCTGTTGGA	ATGTGTGCAT
31601	TTGATGTGCT	CAAGATTAGG	GCACTCTGCT	TGAGAACAAA	TAACAAAAAA
31651	GGGAGAGGAA	ACAATAAAAA	CTTTGGTCCT	ATAAAGCACC	TGAAAGTACT
31701	ATAAATTGAT	GGTTCCTAAG	CTGGTCAGGG	GGTCCAAAGG	CTACAGCCTG
31751	GGGGCCTCAA	GTTTAATTGT	TTTATAAAGT	GTCCTAAATA	AAATTTTTAT
31801	GTTTTTAAGT	GGTATTTTTA	AAACTACTTT	TTCATGCTTT	GAGAGAGTTT
31851	TCCAAATTCC	AATTATTTTA	AGGGGTTATT	TCCTGGACTT	GCACTTAACG
31901	ATTTTGAGAT	GTTTACATTT	TTTTCAATAT	GGCATTCTGT	GTGCCTCAGT
31951	GATACATGGT	TATCCAGGTT	GCATGCATAT	ATAAATGTTA	AGATTTATGG
32001	AAGGTCATCT	TTTTAGATTA	AAAAGAATTT	TTTTAAGCTG	GTATTTCTTG
32051	GTGATAGGGC	CTAGAAATTA	TGTAGAGTGG	CTTACTTCTG	GAACCTATTT
32101	TAAACTGCAT	ATAAACCATC	CGCCTAGTGT	ACAGTTGGCT	AAAGAGTAAT
32151	ATTAGAAGGC	CCTCCTGGAC	AGTTTATTTT	ATTTTCATGGA	TATGAACACA
32201	ATTGTTTTCC	TTTGAATTTA	ATGCCATGTT	TAAAATCAGA	TTTTAAGAAT
32251	TTTCCAAGGG	CATTTCCCTA	TCATTTACAC	TCTGCTTGTT	TTTTCTTTCT
32301	GTAGTCTTTT	ACATTAAATA	CCTCCTACAG	AGCACTGCCT	AAGGATTTGT
32351	GGTGGTACAG	GGTCCAGTTG	GGATGACAAA	CAGGCAAGGA	AGGCCTGGAA
32401	GTAAAATTAG	CAAAGAGGCC	CTGTGGAATG	GAAGGTGAGG	GAAGGGTTAG
32451	TGACAGTTGG	GGGAGGAAAG	GTAGAAAAAA	AAATAACATG	CACATCAGTT
32501	TCGCAGGAGT	ATTAGAGTCT	TAAAGGAAAC	AATGTTTGAT	AATTATCAGA
32551	GAGGAAACTG	GGAGCATAGA	GCATATCCCA	GAATGGAGAA	CAGCATGGGT
32601	TAAAATGGGT	AGGAACAGGT	GTCAGGAGCT	TCAAANNNNN	NNNNNNNNNN
32651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
32951	NNNNNNNNNN	NTGATTTTTA	TCAGGCAGTT	ATGATGATAA	ATGTATGGAA

FIGURE 3K

33001	ACTTCCCATT	TCCTAGAGCT	AAAGTGCATG	TTTCTCATTC	TGAAATGTAG
33051	GGAAACATAAT	CATCTGATAC	CACTCACCTG	ATTGTTTCTC	ACTCTTCCTC
33101	CACCATTTTAC	CCATCTCTTT	AGCTTAATGA	GTCCCTGTG	TATCTCCCAA
33151	CTAAACAGCG	GCTTACTTGC	CTGTGAAATA	TTCTTCTCTT	GGGTAGTCTG
33201	CTCCCTTCTC	TGTCTACTCA	TGCTTCAAGA	TTCAACATAA	GCCTCCTCTA
33251	TGAGGCTTTC	TGCACGTATG	TATATGGATT	TGCTTGTGTA	ATGATTTCTT
33301	CACAGATTTT	ATATTGCTGA	TAAATAAATA	TTGTTTTGAA	TAAGAAACGT
33351	GGTTTTGTAT	TTTTATCTCG	ATTGTAGACT	CCTTGAGACC	AGTACCATGC
33401	TATACAATTA	TTTTTCATCT	ATTATAGTGT	CTGGCATAGG	GACATGCACA
33451	TATTTGGTAC	AGAANNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
33651	NNNNNNNNNN	NNNNNNNNNN	NNNNNTAGAG	AATAAACGGA	ATAAATTCCA
33701	ATTAAACAGT	GAAAATATTT	GAGTGATGAT	TTACAGAATT	TTAAAGTCTT
33751	GAGAAAGTGG	AACTCAGTTG	ATGGAAAAGA	GTGAATGTCA	AACTGAGAAC
33801	GTCTATTTTG	CTATGTTAGG	GCATAGAAAG	GCCATTATAG	ATTGAAAAGC
33851	AGTTGTAATG	AATCTTAGGG	TTAAGAAAGA	TCAAGATACA	GAAATATCCT
33901	TGAATTGAAG	TTCCAAAACA	ATGTTGTTTT	GGTTTTTGTT	TCATTTTGAA
33951	TCCTTTCATA	CTTAGGAATA	CCATTTCTAG	TAAAATAAAT	ATTTTATGTT
34001	TAGTTAGAAA	TTTATCTGTA	TTTCATACAT	ACTTAGTACT	TTTGGACTAA
34051	GAAGTGCTAT	TGAAGTATA	TTTGAGGGAA	TGAGTTTGAA	ATTTTGGGTG
34101	CAGGACATTA	TAAAGTTGTA	ACTATGAATA	AATTTAGTTT	ATGCTTATGC
34151	ATAGTTTTAC	CTAGTTTTAT	TTGTCTATTT	GAGTATTGTC	CTTGAATTTA
34201	AAATTTTTTT	CAGCCCCAAC	TGATACACAC	ACATATACAT	ACATAATACA
34251	TGTGTGTGTG	TGTAGCTTAC	AGAGTGTTTA	TAGGAAACTG	ATTTTGTATA
34301	CTTTGGCTAC	TTTGTTGTAA	GTTCTAGTTT	TTTTTCTTTT	ATTATTAAAC
34351	TAGTGCACGA	CATCAATGCT	ATATGATTGG	TGTTTCGTTG	ACCTAGAAAT
34401	AATGCATGCC	ATCTTCTTTT	CACAGCTGTG	TGCCAACCCAC	GATGCAAACA
34451	TGGTGAATGT	ATCGGGCCAA	ACAAGTGCAA	GTGTCATCCT	GGTTATGCTG
34501	GAAAAACCTG	TAATCAAGGT	AGGAAAACAG	TCTGACATAA	ATACACAATC
34551	GAAGACACCT	CTATCACTCC	CAAATTAAAA	ATATTCTTAT	CTCAAACCTAC
34601	TTTCCATGGC	TATTTTTCCA	AAATATGTGA	GCTGCTATTT	TGCTGNNNNN
34651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTTTTA	TCAAAGGACA
34701	ATTAAACAAA	TTGTATCCTC	TTATTCTCTG	ATACTAATTA	AAATGTATTT
34751	TGAAGAAAAG	AATCCCTGCA	TCAGTAATTT	AGAAGCCTTC	TGGTACTCCT
34801	TGTTTTTCCA	CTAACTAGTT	GGAAATCCTT	GGCCAAATAA	TTAACCACCT
34851	CAGACCCCAG	GTAAGCTTTC	CCTTTAATGC	CAAAGTCAAG	TAGGGGATTT
34901	GATTTGAAAT	TTGGAGTTTC	CTCCTAACTC	TGAGCCCTTC	GATTCGTGAT
34951	TAAATCTCCC	TTCAACTACT	GACCAGTTTG	GAATGTTTCC	ATGATAAATA
35001	AAAATGATTA	ATTTAGCAAG	CACTTTTTAA	AAAAATCAGC	ATCAGTTGTT
35051	TAAAGCAAAAT	ATTATTCAA	CACTCATAGT	GCCCCAGGTA	TTTTATATAT
35101	ATAATCCATT	TTTATCTTTA	CAACAACATT	AGGAAGTAGA	GCATTATTTA
35151	TTATAATNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35301	NNNNNNNNNN	NNNNNTTTT	GGATAAAAAA	ATATATTTGG	AAATGTGATC
35351	CTCGAACTCA	TGCTACAAAG	TCAGACAAGG	CTGTCTTGT	TAATTAAATT
35401	CAGTTAAAAA	TTTCCATTAT	TNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NCATTATTAG	GAATTAAACT
35751	AAAGAAAAGAT	TAGGGTTAGA	TTTCACTAAA	TAGATAAGTG	TCAAAAATAA
35801	AAAAGATAAG	TCAATTTTTA	CTTATTTTTT	AAATTATACT	CCCTATCATC
35851	TTAAATGTCA	GGTGAAATAA	TCATGGTGTC	TAATATCCC	TTACATACTT
35901	ACTTGACCTC	ATCTGATATA	GAAATGATAT	TGCTGAAATA	CTACTGTTCT
35951	TCAGTGCTCG	ATACTTATTC	CAAGATACTC	CTTGAGGTAT	GTCATGTAAA

FIGURE 3L

36001
36051
36101
36151
36201
36251
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36851
36901
36951
37001
37051
37101
37151
37201
37251
37301
37351
37401
37451
37501
37551
37601
37651
37701
37751
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37851
37901
37951
38001
38051
38101
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38751
38801
38851
38901
38951

36001	CTAATGATTT	ATAGACACAG	TTTTTTTTTC	ACTATTTATN	NNNNNNNNNN
36051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
36301	NNNNNNNNNN	NNNNGACACC	GTTTTTACAA	TCATCCAGAA	CATTGATTTT
36351	TGAAAACATA	CTCAAAATGG	TGGTTCATGA	ACCATCAGAT	GAAATTATTC
36401	ATGAACCATC	AGATGAAATC	CACACTAGCA	AAAATGACAT	GTCCCAATGG
36451	TAGAAGCTGC	TATTCTAAAG	TGTGTTCTTG	TATTATCTGC	TATTTGATTT
36501	AGAACTGATT	TTCCCAATGC	TTGTTTTCTC	TCTAATACTC	TTTTTAACTT
36551	GAAATTTACC	AAACATACCT	GCATAATCTT	TTTAAATAAG	TGATGCTCTT
36601	ATTATCTCAG	TTTGCTCCTT	AAAAAACTCC	ACTTGATTTT	TCTTCCCCAG
36651	CATAAGTTTG	CAGGTAGCAG	TGTTCTGGTT	ATTGGATGCC	AATGTTTCATC
36701	TTAGAATCTC	AGTATACTTT	TTTTAAAGTG	GTGAACATAA	GCCCTCAGAG
36751	GTTTCATTAA	TATATCAGCA	CGGTAAAATA	TTGTTGTCCA	AATGTGAGGA
36801	TATAAAATAT	AAAGAAGACG	ATTAAAATAA	GTCACTTTTG	AGATTGCAGA
36851	GAAATTCATT	TAAATTTCTT	TGCAGAAGCT	GCATCAACTT	TAACATGCTT
36901	TAAAGACATG	CTAAAAGTAT	TATTGAAACA	AAAGTTCATC	ACTGGGTAGC
36951	TCCTATTTTC	AGAAAACCAG	TTTAACATGT	ACTTTTTTTT	CCTGTAACAC
37001	ATACCTATTT	CTCTAAAGAA	AAAATCGAAT	GTATCAAGTT	AAGATCTTGC
37051	TCCCCAAAAC	CATATTCCTT	AAAGAGAAGA	GGATTTGATT	AGTAGCAAAA
37101	TGGGATTTTA	CACCTGCAAA	AATAGTGCTG	ACACTGAAAA	TGTAATTTCA
37151	AGTCCAGTTT	TGAAAAATAA	ACTACAGCTT	AAAATAAACT	TAGGTGTTTT
37201	AATCATCTCT	TATTTTGCCC	TCCTCACAAA	AAAGCAGTGT	GGCAGGTTCC
37251	TGATGCAAG	GTTNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
37301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
37351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NAGTTTCATC	TAATGGTTCT
37401	TAGTCCTGAA	CACGTGGAA	GCTTGAAAGG	GTCCACCAG	TTCTTGGTAC
37451	AGCATCTTAG	AGAGTCTCTG	CATCCATAGA	CTTGAGGGCC	CTGTCAGGAT
37501	CAGGGAAGCT	GCCATGTGTG	GCCTGGTTGA	GTGTGAGAGC	TGCCTAGAGA
37551	CTTCATAAAA	AGTTGTTAGA	GAAAATTGTT	GATAGTGCCT	ACATAGCAGA
37601	TTAACTTAAA	CTGTTTTCAT	TCAGGCCAC	ACATTTTAAT	AAAGTAGAAA
37651	ATATGCTTCA	CAGATAAGGG	AAATCAAACA	GGCTCCTTTT	TTCTGGAGGA
37701	GAGAAATGTC	AAAAAGAATT	AAATTTGAAA	TAACTTTACA	GAAGTGGAAA
37751	TTAGCTTTTG	ATTAAAAGTA	GCTTTTGGTA	TATGACAGGT	ATTCAGTGAG
37801	AATTTTGTAG	CGAGTTATAT	ACTTTAAGAA	ATAACCCCCA	GAAACTTGCA
37851	TCATGGTGTA	AACAGCTTGA	ATAACAAGT	GCTTAACCAG	TGCCTTTAGA
37901	GCTGCCTGGG	AAACAGCCAG	AATACCAGGG	CAAGCTGCAT	TTTGGAAGCTG
37951	GTTTAATTTA	GTAGCCTTGC	CACAGGCTTA	GTGTGATCTG	CTTTTGGTGG
38001	CTTGATCTTC	CCCCTAAGT	CATTTTCTGG	ATTTGTTACA	CCTAGAAGCTG
38051	TTAGGAAATT	ACAGCTTGG	GCTGATCATT	AACATACGT	ACTCTACAAG
38101	GCACACGTTA	CCTTTCAAAG	CAGATGAAAT	TCTAACCTGA	ATTCTGGCAA
38151	GATTCTTTGA	TCATTTGCTT	CCTTTACTTT	TACTTTTATT	TATGCATATT
38201	TCCCTCCTCC	TTGAGTTTCT	GTACCAACAC	AAACCTCTTT	TTCCCCCAGC
38251	CAGNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NTTTTCCATT
38301	GGGGAATGAT	TTTTAGTATG	TAAATATATC	ACTGCATATT	CTCAGAAATG
38351	AAAGACATTC	TTAGGAATTT	ACAGTGACT	TTATAATAAT	TTCAGAAAGAA
38401	AATATTTATA	AATGTCAATT	CCTAATGTTT	TAGCATGGTT	TATGTTTCAT
38451	ATGTTGAATT	CTTTATCATA	AGGAAAGAAT	TGGAGTCTTT	TAGGTCAGAA
38501	CCAGATACTA	ATTTTGTGGA	CTAGTTACAT	CTGAAAGTTG	ACTGCTTTGC
38551	TAAGCACAAA	AATCTAAGGG	CTTAACTCT	AATATTAAGG	TGTTTACCTA
38601	CAGCCGTAGG	TTTTGAAAGA	TGTATGGTTC	CNNNNNNNNN	NNNNNNNNNN
38651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
38901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNGAAG	TTGTATGCTT
38951	TCAACTCCCA	AAACCAATGT	TCATTTGATT	TGGACATTTA	ACTGGCTATT

FIGURE 3M

39001	AATAACATAA	TGGTGTGAA	ACAGAACGTG	ATTGTTAAGT	CTCAACTCTC
39051	TTCTTTGAGT	CTCACCCATC	TTATATTTTG	GTAAGCTAAT	AATGGCAACA
39101	GTTAACATTT	TTTTGCATAA	AGCTTCTCAT	GTATGTTCCA	GAAGCATAAT
39151	TTCTTACATT	TAAATGATAA	TATTGACGAT	CTATTATGCT	GTTATTTAAA
39201	TAAAATCTTT	ATGTAAATCA	TACATTTGTG	CATAATTTTG	GAGTATTTTA
39251	AACTACTATT	GTACAACGTG	ATAGTGTAGG	GAAAAAATC	TTAAGTTGGT
39301	CGTTTACAAT	TCAGTGTCC	TAAATAGAGC	AGGTGGATTA	TAATCAATAT
39351	TTGTATAAAT	TGTTTTTGT	TTTCTTCCTT	CTGTGTATGA	CTAAATAATA
39401	CTTTTAAAAA	TGATGATCTC	TTGTTTGGA	TTTTTTAAAA	AATTGTATGA
39451	CGATGGATTG	TTCATTTATA	ATGTGTGTGT	TGTCCTTGGG	AAACAAGATG
39501	ACAGTGATAC	ATTTTAAAGA	AAATTAAAGG	AAAAGAGAAA	CCAGAAGAAC
39551	CAGAACTAT	TGTTTATAAA	GTATCTAATG	CATTCTTTTT	AAACTCTACC
39601	AACTGTATGT	AATTGTTTTA	TATATACTTG	CAAAGATTTT	TAGGGCTAAA
39651	ATTGACATCA	GTTCAAAGTT	GACTCTTATT	ACCTTCTTCC	TGGTGTGAAG
39701	ACGAGCACAT	CCCAGCTCCT	CTTGACCAAG	GCAGTGAACA	GCCTCTTTTC
39751	CAACCCCTGG	ATACCAAGC	CACAAGTTTG	CCTTCAAGGG	GTGACGTGC
39801	ATTGTCCCAG	GTGGTCTGCT	CTTCCCACCT	GCATGGCTTC	CTGCAGTTAT
39851	GTCACTTCTT	GCAAATGTTT	TGAAGACTAG	CCCAGGAGTG	TCCAGCCTTC
39901	AGCCTGAGC	ATGAGCAAGC	AGCAGGAATT	GCCACCTGGT	GCTGATTCTC
39951	TGTGCTCTGA	AAAGCATGGA	GCCCTACTGT	CCTTTTAATG	CATCGAGTAT
40001	CATTGCTTTT	CTTCTCTTTT	TCTGAATTTT	GAAATATGTT	CTAAAAACAG
40051	ATAGCAAAAC	AACCTTTTTT	ATATGTAGGC	AAATTCAGGA	GTTCCAAAGC
40101	AACTGAAATT	GGGGGTTTGA	TGCCTTTTGC	CAAGGAGATT	TTAGAAATCA
40151	AGTCCTCTTC	CCCCTCTTTC	AGGTATAGAG	TTTTAGGTTA	TCTGAAAATC
40201	AAAGCATACA	TTAGTGACCT	TCTTTTGGTA	TACATTGTGT	AACATCAGAT
40251	AGCCTAAGTT	CTGGTTCCAA	GAGAGCACTT	AGTTGCTATT	TGATTATAAG
40301	CAAGTCATTA	ACCAATCAGT	AACAGGGAGA	CAGTAATTCC	TGCCCTATTT
40351	GCCTGTGGGG	TTGGCGTGAG	AATAGAAACA	CCAAAAATAT	TAATGTCTTC
40401	GTCATGCTGG	AAAGCTTTGT	AGGAAAATAA	TGTGGTAGCA	TAATTTTACA
40451	GTTCTCTTTT	TAGGTCATTT	TATCTCTAAC	CCATTCATAG	GTTTAAGAAC
40501	TTAGAATAAC	TGAATTAATA	TAGTTGAAAT	TATTAATCAT	TGTCTCTGCT
40551	GAGAAGAAAT	TTGATGCATT	TGTATATTTT	CTACACAAGG	AATTAGGGCA
40601	AAAGAATTAA	TTTCGGTCCN	NNNNNNNNNN	NNNNNNNNNN	NNNNNGTAGT
40651	TGACATATTG	ACATCTGTTT	GCCTATGACA	TTGCCCGATT	TAAGCACCAA
40701	AGCGGGGAGA	AAGTCCAAAT	GTGTTAAAC	AAATGAAAGT	TTATTTTAA
40751	AAAAATCCAGT	AAGTTAGTTA	TCTCCCGATT	TTTCAAGCTA	CTTTTCAGTG
40801	TCTGCATGCT	AATAAAATTT	CTGATTTTTT	TCCTGAAGTT	TAATAATAAT
40851	GCTGTGCAGC	TTGCATTTCC	ATTCTGGACC	AGTTCCTTTC	TCCCTCTCCT
40901	TCTCCCATCC	AAGCTCCTGA	ATCCACCAAC	CTACTGAAAT	GTATTCCTGA
40951	CAATAGTAGA	TGCACTTTAA	GACTTGTATA	CATAATAACT	GAAGCATTTG
41001	AATGTAAGTG	TTTTATTGTA	AAGTTCTATC	CTTTAGTGTA	AGATAAGCAC
41051	ATGAAATAAT	GCTTAAAT	TTTATTTTTC	CTATTTTATA	GATTTTCCTT
41101	ATATATATTA	TAAACCTCCA	GAGAAAAAGG	AAGATAAGTA	AATTTAAAAAT
41151	AAAAACACCA	AAGTTTTATT	TCTAGGTTCT	TTTATCAACT	TTTAAGATTT
41201	ATTTGAGACA	GTATGATCAA	TGACTTCATT	TTGTTCTGCT	TATTATTGTA
41251	GGAGTATTTA	CTATAATTTG	GAAGTAATTT	ATTTTGAAT	TTATTGCTTA
41301	ATTGAATGAT	CTCCAATAGA	TTGTGATAAT	GAACACAGCA	TTTATAGAAA
41351	GCAGCACATA	TTAACTTACT	TAATATGGCA	CTAGGTCAAT	GAGAAAAGAA
41401	GGTAACATAA	TTGAAGACAA	GAAACTCTTA	AGAAAACTGA	GGACAAAAAG
41451	GCTTCTCACC	AGGACACCAG	ATGCATTTAA	TCTTTTGAAG	CTCTGTACTT
41501	TAGGAAAAGT	CTGATATTTG	GCAAATTTTG	ATAAACATGG	ATGACTATGG
41551	AATCCTATTT	TATAGTATCT	GAAGTGGCTT	TCATAAGGGT	CATTGTGAAG
41601	TTTTTAGGAG	ACACCTGCCT	GTGGCAGATG	GGACAATGAT	GGCAGTCACT
41651	AGTGATATTA	ACACCAGTCA	GCTGTCAGGG	AATATCATCC	AGACCATCAG
41701	CAGCTGGTAG	AGTACAGCTT	TCTCAATTGC	TTTCCATGTT	TTGGATACTT
41751	ATATGCCCGT	TAATAACAGG	TAAAAATAGCC	AGTACATCAT	TTCCACATTT
41801	ACCCATTGAA	TGTTGCATGT	TTTCTTCCTT	TCACATATTC	ATACAGTCCA
41851	GATTTTTTTT	TGGACTCATG	ACAGCACATT	GGCTTTTCTT	TCCTTTCAGT
41901	TTCATGATTC	TTAACCCCAA	AGTGCTTTTG	CCATGGGAAC	GGAAGGATAA
41951	ATTTGCGTCG	AAGCATTCTT	CTAAAACCAC	CAGCAGCTCC	ACTCCAGATT

FIGURE 3N

42001 ATGAATACTA CCATAGCAAT CCTAAGGGGC CCTTTATTGG CCCAGACTGG
42051 AGCCAAATTG TAGAAGAGCT GCCCAACTG GGCTTCAGGT TTAGTTCAGG
42101 GACATAGTGT CTGAAGAAAT TTCCATCAGC ATAAATACTC CTTGTTTATG
42151 AGCTGCCTGA AACTGTAAAC ACCGAATCCA TTCCCATCAG GAACTCACAA
42201 AAGTTTCTGT TATGCTTTGA AAATAAACCT AGGGATACTT AACTGACATG
42251 TAAAGAAAAA TCCATCAGTA TCCTTTTCTC GAGATATAGG TTTTGATTTT
42301 ACTGTGTTAT GTTGTGGTTT TGTCTGTTT TTGTTTAGTG CAGAAAAATA
42351 CTTAAAAACAC AAAGCCTTTC TCTAACACCA TATTTGGTTT TAAATGCTAT
42401 TTGCTATAAT ATCAAGAAGA TTTATCAAAG ACAGGTGTGA CTCTGCAGGA
42451 CCATATTAGG AACAGTCATT AACTCCTCTT AGAAGATGAG AAAAGTTTCC
42501 CTCTCATTTT TAGTAAATTC TGAAATACAA AGTAGAAGAA TATGGGAAGG
42551 GTAGAAAATT TCTCAGTCAT TCTTCCTTGA TTTTGTGCTC AATTAACAGA
42601 GGGAGAAAAC ATTTTGTGATA CTGTAATCTG CATGGCGCTT TCTGTGAGGA
42651 AATTTTTTTT GAAATATTTA AAATGTGATT TTGTTTTAAA AACCCCTAAC
42701 TAGTCAAGAG ACAATAAAGT AGAAAATTGA AGAACGCATA GGAGATGACA
42751 AAAGTATTTG GTTTATTTAT TTAACCTTTC CGGGATTGTC CCAGCTCGGG
42801 GTCTGCTTAC AGTTGCATTC AGGGCAGATA AAAGACCTAC TTGGAAAATC
42851 AGTAAGATAT GAAAATTTTT TTAGATGTAA TAATTATTTG GTGGTTTTAA
42901 AACATAATGG AACTTGATGA TTTAGTTAAA TGAAATATAC AGATTTCTAA
42951 TAAATGAGCA GATCAGATTG AAATAGATTA GATTTGAAAA CAATTTTTGT
43001 CACTAGACAT ATTATCTATA TTTTATTTC AATGACATGG ATTAATAGAT
43051 AATTAAATTA TGCTAAATGG GTACTTATGC TGGTGGTTCC AGACAAACAT
43101 GTGGTCACAT TTCTTTTTAA TGAAGCATAT ATTTGGGCA TTAATTTTC
43151 AATGTTTATT TGTCATTATG AGTTTATGT TCACTTGAGG CAGTGTTTAA
43201 TTTAGGTAA AACCTTTTCA TAATGTAAAA TTTGTTGATT CATTTTCATAT
43251 TGATACTTAA ACCAATAAAC CTGAAATACA TGACAGTCTA TTACATTTTG
43301 TCCATTAGTG TTTCCATATG CCTTTTTTAA CTGCGGAATA AATGAAAATA
43351 TGTGGTAGG TTTTTTAAAG TTCATTTTGT GACTTGAATG CATTACTAAA
43401 GTAGGAAACT GAAGTTTCTT CTTAATCTG AAATCATATA AAATCTACCA
43451 GATTGAACAA GAAAAACTAC AATATTGATC ACTCTAATT TATTTCTGTC
43501 TTATCCTCTG AAAATATAGC CTATGTAGCC TTCCTTGGG ATGGGAAGGT
43551 CAAAGCAGTC AAATGTTTTA AAATCTGTAT ACTTCCTGTA AAATAAAATA
43601 TTCTCAAAGT CCAAGCCTTA AGGAGGCCAA TGCCTTATCC ATTTAAAGTA
43651 AAATATTCTC ATGTAATATG TTCTTTAAAC AGAGAAAGGA AGACATTGAA
43701 CGAATAGGGT TACATTGTCA GGATTGGATC TAGCAATAGA ACCCAATAT
43751 TTTGAGAATA TTGGCAAACA GTTGTAGCT GATAGAGCAT CTCTGCCAT
43801 GAGGACGTTA GTATGCTGCT GTTCTAGGG TTGATAAGGT AGGCACCTGT
43851 TGTTGAGAAT TTTCTAACT GGCCTTTATA AACAGAGATC CATAAAGGTC
43901 ATGGCGACTC CTGTTGCCC CTAGTGTAAC GTACCTTCAA ATTAATATTG
43951 CATGAACAGG ATCTATCTCT TATGTAAATG ACAGTTACTG TAGCTTGACC
44001 TATTTTTCTC TTTCATTTTT TAATATAGAA AAGAATTTTA GATGGCTTAC
44051 ATTAGTGCTG AGTTTTGTGA ATTTTCTGC TTCAACCAC ATGGTTTTCA
44101 GATCTAAATG AGTGTGGCCT GAAGCCCCGG CCCTGTAAGC ACAGGTGCAT
44151 GAACACTTAC GGCAGCTACA AGTGCTACTG TCTCAACGGA TATATGCTCA
44201 TGCCGATG TCTGCTCA AGTATGTCAA GAATCTTAA TGTTTTATAA
44251 GTGCTTTGGG CTGTTTCTG TTGTGCTCTG AGAGCTTGCT TTTGTGAAAA
44301 TGGCCTCCGG GGTCTCCTA AACAAGATGT GTGCGTGTGT TTATACTTTT
44351 GCCTGAGGAA TTGAAAATCA AAATAAGAGG CACCATTTTC GATGTATAAT
44401 ACTCTTCTAT CACGGGTGCC AATATTAAAT TGATTAGGAA ATGGTGTTTA
44451 GAATAAGAAT TACAAAATA AGTATGTTTT CTAATTTTTT TTTTAAACAT
44501 GTTTACCCAT GTCTTCTATC TGGGCATAGA AGAATGATTC CAGGCTAAAA
44551 AAAAAAAAAA AAGAACACTA CTGACTATTT AGGGACTGCT CAGACAGAAT
44601 CCATCAGGTC TGTTTTGTAA TTTTAAATCA TTCATAAATA TTTTCTTCAT
44651 TTTTATATTT CATTATAAAA GCCTTTAGGC TTTTATAGAA TTTTAGACTC
44701 TAATAATAGT CTAAGACTTC TAAAAACAA TTCAAATAA AAAATAAATG
44751 AATATGATAC CAGAAAAGTA GGATTCATGT TTATAAGGAA GAAATGCATG
44801 TTTTACCAT CATTTGGATG TAAAAAATGG ACTTTGCCCT AAAATTCTCT
44851 ATAGGCTGAC TCCTGAATTG TGGTATTCAT ATGATATCTG ACAATTAATG
44901 ACTTGATTTT TATTTTTACT GAATTATCAT TTAAGTGAAT TGCATAAAAT
44951 AAAGTTAGCT AATTTTTATT AACATTGCAT AAGTATAGCA TGGAACTTTT

FIGURE 30

45001 45051 45101 45151 45201 45251 45301 45351 45401 45451 45501 45551 45601 45651 45701 45751 45801 45851 45901 45951 46001 46051 46101 46151 46201 46251 46301 46351 46401 46451 46501 46551 46601 46651 46701 46751 46801 46851 46901 46951 47001 47051 47101 47151 47201 47251 47301 47351 47401 47451 47501 47551 47601 47651 47701 47751 47801 47851 47901 47951

45001	TGGAATTAGG	TGAATACATG	TTTAACATTG	TGCAACTCAA	TGGGAAATCT
45051	GCTGTTCCCC	TAGAGAAATT	TCATGGGCAT	TTGAGACAGT	TACTTGGATG
45101	ATTAGTTAAG	AATAGCGTTT	AGCTTGAGTA	ATCTGGAAAA	ATACCTCAAT
45151	TCTTCACTTT	CCTTGGCCAC	TGGAAAAATT	TCCAGATAAT	CTATATATGA
45201	TAGTTTTATA	TTTGCTTTTT	AATGCTTTCT	TTCCTTCCCC	CTTTTATTTT
45251	CTTTAGATGT	TTGATAGTTA	AGGCCTCTTT	GTCTTCATTG	TTGTTCAGTG
45301	TCACTGATTT	CAGGACAAGT	GAAAAAACAT	AGCTATTTCC	ATTACAGATT
45351	TTGTTTTCTA	CCTGTCTGAG	TCAGCCAGTC	ACTCTCTTTC	CAGGTGCCCT
45401	GACCTGCTCC	ATGGCAAAC	GTCAGTATGG	CTGTGATGTT	GTTAAAGGAC
45451	AAATACGGTG	CCAGTGCCCA	TCCCCTGGCC	TGCAGCTGGC	TCCTGATGGG
45501	AGGACCTGTG	TAGGTGAGTT	GTAAATCAA	GCATCTCTGT	CAGCAGCCTC
45551	TGTAGGATAA	AGGGAGAAAG	TGAAAGGTGA	TGGGAATAAG	GAAAAAAAAG
45601	GCAATTACTT	ACATCAGATA	ATTAGCTATC	GTTCAGAAGA	TATCAGATGT
45651	CTCAGAAGAG	GACATCTCTG	TGAATGGATA	ATGGGAGCGT	TGTTTTTTAA
45701	AAAAATGAGAA	ATANNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
45751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
45801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
45851	NNNNNNNNAT	TGTATGTGTT	GTTCTTCAGG	CCTCAGATTT	TTTTCTGGTA
45901	AATTAGGAAG	GCAGTGTAGG	ATTGAGAGTC	TGGANNNNNN	NNNNNNNNNN
45951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA	AGTGTGTTGGT	GATTAGAGTN
46151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
46301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNGTCTATT
46351	AGCCTTAAGG	TAAGACCTGT	ATCATTAGCC	ATGTGAAGAA	ACAGCCAAGC
46401	AGCTGAAGAC	ATTGCAGGGC	ACTGCGGTGA	GAGAGAGGTT	GGCCTGTGTG
46451	AGGTTTTTCA	AGGAAGAAGG	TCCATGTAGC	TCAAGTACAG	GGTGTGAGTA
46501	TGAGGGGTGG	TGGCTGGAGA	TATAATGGGT	GAAGTAGGTG	AGGGTGATTT
46551	GTTGCAGGGC	CTTCAAGGAC	ACAGGGGAGG	AATGTGGATT	TAATTCAAAG
46601	TGCAAGTAGA	AATAGTTAAA	AGATTTTGAG	CACAGTAATG	ATCTGATTGT
46651	ATGTTTTAAT	GGAATCATTT	TGACAGTTGG	GTTGGATATG	CTTTGGAGGG
46701	GGTAAGTAAC	AGCAAAAGGA	ACTGTTTTGA	GGCTTTTGTA	ACAGTCTAAC
46751	CCAAGAGATG	TTGGCTTCAA	ATAGGGTAGT	GGTGGTGGAT	TAAGAGAAAA
46801	GTAGACAGAT	TCAAATACTT	TTTTTTAGAG	GTAGAATTAA	CTGGACTTGA
46851	TGATATGGGA	GTTAAAGGAA	AGAGGGTTGT	TTCTAATTCA	AGAATGACTC
46901	ATGTTTCTAG	TTTAAGCAAC	TTGGTAGATA	CAGGTGCAGT	ATGTGCTAAT
46951	ATATAGAGTG	CAAGAAAATA	ATAACTTGGC	TTAGAAGGCT	GGGTTGAAAT
47001	TTGGATATGT	GGAATTTATG	TTGCCTGTAG	GGACAACCAG	CTAGATACCG
47051	TTTATGATGA	GCCACTATAT	GCTAGGCAAC	CATTTGTAGT	CAGTTATTTA
47101	TTTTGAAACC	CACCTGTGCT	TAACATACCC	TTGCTCTTCC	TAAAATGCTA
47151	TTGACTTATG	TTTCTAGATG	TTGATGAATG	TGCTACAGGA	AGAGCCTCCT
47201	GCCCTAGATT	TAGGCAATGT	GTC AACACTT	TTGGGAGCTA	CATCTGCAAG
47251	TGTCATAAAG	GCTTCGATCT	CATGTATATT	GGAGGCAAAT	ATCAATGTCA
47301	TGGTAATGAA	ACCCAACCAT	TGCTTTGTGT	TGTTTCTTCC	TAGAGCACTG
47351	AAAGGTCTCG	TAATTGTGGT	GATGGCTGGA	ATGTCAGGGG	CAGGGGAGAG
47401	TACTGGCGTT	AAGTTAAACC	AACAGACATC	CAGTTTAACC	ACTGGTAGTT
47451	CTCAGTCTAC	ATGTAGTTTA	TTTCTTCTGT	TTATCTGCCA	ATTTTATGTA
47501	GATCATCACA	TTGCCAAAAA	AAATCATTTT	TGAAACTGTA	TATATTTTTT
47551	ATGTCATCAT	ATTTATCTCC	TAAATAAGTC	TCTTCTTTTC	CTACTTTCTG
47601	ATGCAGACAT	AGACGAATGC	TCACTTGGTC	AGTATCAGTG	CAGCAGCTTT
47651	GCTCGATGTT	ATAACGTACG	TGGGTCCTAC	AAGTGCAAAT	GTAAAGAAGG
47701	ATACCAGGGT	GATGGACTGA	CTTGTGTGTG	TGAGTAGCAC	TTGTCTCTCA
47751	GCTTTAAATT	CTAGCAGGAA	ATACAGGATT	ACACAAAGGC	CATTGCTAGG
47801	GAAAATAAGG	AATAAGATTA	TCAAAGAAGT	ATAATTGTCA	TAATTGGTTA
47851	TATTTGTCTT	TGATTTCCAC	AAACAATAAA	ATCACTTGCT	CAGGTACTTG
47901	TAAAAACTAA	GGACTCAGTA	ATACACTATA	ATCTTAAGAG	TATTTTAATC
47951	TCTTCACTGA	AATCTCTCAA	TATTTTCTTT	TTAGCTAAAA	AGAAATTATT

FIGURE 3P


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48001 GAGTCCTCCC TGAGAAATTTG CTTTGTGTTAA AATTAGAAAT CATGTTTGCC
48051 ATTAGCGTTA GATTTTGATG GTGGGATAAT CTGGATATAT TCTACATTTT
48101 TTTCCCTCTG TTTTATGCCT CCTAACTCTG CTATTAAAAA ATCATTCCCN
48151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
48451 NNNNNNCCAT TCCCATATTT ATTCCTCTA CATTCAGAAC TGTTTTGCTT
48501 TTAAATTTT TATAAGTTT ATTTGGAGTA GTGGTTATGT AATAGATAAA
48551 CATGAAAAAA ACCCAAAGT CATAATTTAA CACATTTTC ATGTAACAGA
48601 AGATAATTTT TTAAATTTCC TCCGTAAAAT ATTTACTGAA AACCATGGTG
48651 CATAAAATCA TGAGGATTAA AGGGTTTTTA AAGAGTCATG TAGTCATTCC
48701 CAGTCTGGAA TGTATCATTC AGGCAGATTA AATATTGATT CTTTTTGATG
48751 AAGATTATCA AGGAAAAAGA TTTCACAGAT GATCTTTGCA ACCTCTGAAA
48801 ATGTCTATTT AAAAGCAGTT GTATCTATCA GTAAAGGGAA ATAAAAACCG
48851 ACCATAAAAC AATATGTAGA ACATTTACTC AAGCTGTATT TATGCAAATT
48901 GAATTTATAT AAAGTGTGGA TAAGAAAAGT ATTTGTCTTT AGACAATTCT
48951 GAACACAATT TTATAATATA CACGTAGCAT AGGGATACAA CGTAGATTCT
49001 AACTATGCAT TTGCTTATAT TAAAAAACT TAGANNNNNN NNNNNNNNNN
49051 NNNNTCTGTC AGTGAATGC TTCACTTTTT AGGGAGGAAT GGTACATAC
49101 TGATTTAAGT CTTTGACTCT TTCAGTATAT CCCAAAAGTT ATGATTGAAC
49151 CTTCAGGTCC AATTCATGTA CCAAAGGGAA ATGGTACCAT TTTAAAGGGT
49201 GACACAGGAA ATAATAATTG GATTCCTGAT GTTGAAGTA CTTGGTGGCC
49251 TCCGAAGACA CCATATATTC CTCTATCAT TACCAACAGG CCTACTTCTA
49301 AGCCAACAAC AAGACCTACA CCAAAGCCAA CACCAATTCC TACTCCACCA
49351 CCACCACCAC CCTGCCAAC AGAGCTCAGA ACACCTCTAC CACCTACAAC
49401 CCCAGAAAGG CCAACCACCG GACTGACAAC TATAGCACA GCTGCCAGTA
49451 CACCTCCAGG AGGGATTACA GTTGACAACA GGGTACAGAC AGACCTCAG
49501 AAACCCAGAG GAGATGTGTT CAGTAAGTCT AATAAATGTT AGCACATTTT
49551 CAATAGGCTC TTTATAATGA CTTTCAACC ACAGGCCATG CCTTGAATAA
49601 GAATGAAACT CGTAAGAAGA ACTAGCTATG TAAAGTCGTA TGTCCCTATT
49651 GACAAATATT ATAAAGAGCT ACATAAAGAG TCAGTCTAAT TGGGCAAGTA
49701 AGAAGAATG TATGTAGCAA TGGAAGGAAT ATTCACAAAG TCATATGGTA
49751 GATGACAGCT CTTAGCCAGT ATGGGAATTC TGACATAGTT GGATTTACTT
49801 GAAACTCTC AGAGGTGGGA ACTTAACTGT ATTCCATGCT ATGTTACTTT
49851 TAATCTAACC CTTNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
49901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
49951 NNNNNNNNNN NNNNNNNNGG TGGGAAAGAT GGTACTCAG AAGATACCAG
50001 TGGTAGTATG TTAGTGAAAG AGATCTGTGT AGGACACTAT GAGAGGAGAA
50051 TGAAGGGATA CCTCGTCAGT CTTGGGTAG GGAATATTCA GGGAGGGCTT
50101 CCCGAGTGAA ACGGAGCAA GTGGATGAGG AAAGGAAGAT ATTATAGTTA
50151 ACAGGGACAG CCCAACAAAT GCAAAGAAGT AGGAAGCAGT GTAATAGGCA
50201 GTAGACTGCC AGTAAATTGG AGGGTCATGT CAGGGACAGA TGAGAGAAGC
50251 TGGACAGCTA CCCCTTGAT TGCTGTAAAC TGATAGTTAG ACCTACACTG
50301 GGGCTGGATT AGATCAAAGA CTCCAGATT CTTAGCAGGT GACTAGGTAA
50351 AGGGTAGCAC CACCAATGGA GATAGAGGAT TCAGGAAGAG AAGCAAGTTC
50401 TGAAGGAGGA AAAGGTTGTT AATTTATTAC CAGACCAAAA TTGTCATGTT
50451 ATAACCTTCA TCTGTTCTC ATATTTATCT GCTGTCTCTG TGTCATTCTG
50501 CTTATTCTTA ATTACCTTTG CATTCACTCT TCCTGTCTCC TCCTTTATAC
50551 ATTACAGTT TGTTTGTTC CTTTCTCAT TCCTCTATGA TGAAGCTAAA
50601 GTTTGTGCCT TTTATATTGA ATACCTTTAT AACTTTTTAT CAGGTGAAAA
50651 AAATACTGAC ATTTATTATT CTTTAAAGGG GAAAANNNNN NNNNNNNNNN
50701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
50751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
50801 NNNNNNNNNN NNNNNNNNTA ATAAAGGGGA TATCAGAGCC GCATTTTGCT
50851 TGTATGTGAC TCTCAATTAA ATTTCTCCT CTGGGTAATT GTCCATTTAA
50901 AGAAAGAGGG AAATCTCTA ATTCTGATAT AGTCATGTAT GTTTTGATA
50951 ATCAATATAA TTTTtagggg AATTAGATGG TAGCTCTCAA AATATACATT

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FIGURE 3Q

51001	TTATATGTGC	ATAACTATTT	TCTGAAATTT	ATGTTTTTGT	AATTTTCTCC
51051	TCACCCCTC	TCTCCATCTC	AGATACTGTC	TTTTTCTCCC	TATTACTCTC
51101	CTTTTTAAAT	TCTCATCATT	GTGATCATA	AATGGGATTT	TTAATTTATG
51151	AGTGCTTAAG	TAATTATGGT	ATTTACATTA	TTTTGCTGCC	TTAGGATAAC
51201	AGGGAAATTT	GGCTATTTAA	TGTAAGATGA	TACGCTAAAT	ATTTTTTTCA
51251	TTATGATGAA	AGAATACATC	TTTCTGAGAA	TTTAAAAAAA	TCCTTTCTCT
51301	TTTTAAATG	TTTCTCTTTA	TTTCCAGTAT	TCCTCTCTAT	GCCAATACAT
51351	ATATGAATTA	AAAATGACAT	TGAAGTTCAC	CAATAAAATT	TAGTGCAATA
51401	AAATTGGGGA	AATACAGAGT	TCCAATGATG	TTTGGGAGCA	TTCATTATAA
51451	GAGAGTGTGA	TCTTAAAGAC	ATGCTCTGGG	AAAGCATTGC	CTTGATCAAA
51501	TGCCAAGGCT	GTTGCATGCC	ACAGATAGCA	TTGCTGCCTT	TAGAAACTCC
51551	TGCCAAAAAT	TAAATTCAC	TCTCATTTCA	TCTTCAGCGA	TAGCTGCTTA
51601	TTAAGTCTAG	CATGTGTGAG	AATGCTTTAG	ATGCTTTTTG	ACTTGCTGTC
51651	TTGTGGTTAT	AGCATATATT	CTAAATAAGG	CAAAGGCTCT	AAGTTTTTAA
51701	TTCAGGACAA	ATAACCAAGT	TCTATTCAT	GTGAAAACAG	TAAGGAACCT
51751	TAGCACTATT	TCAGTTCAC	ACCATTTCTT	TACTGAATAT	TTTCTTCACT
51801	TCTGGCATAA	CTTCTTAAAT	CATCCTCATT	CTCCGAGACA	GGTCTGAGAA
51851	TAGAATTTAG	CTCACCTCAT	TTCATAAATT	TTTAGGTGAT	GTTAATTATG
51901	GCCACTATTT	GGCAGTCTCC	TTCAAATAGC	CCTCCACTTT	GTGTTTTTCT
51951	TTACATTGAA	AGATATTTTT	AAATTGANNN	NNNNNNNNNN	NNNNNNNNNN
52001	NNNNNNNNNN	NNNNNNNNNG	AAAGATTTCT	TTTAATGGAA	GAGGTTGTGA
52051	AAGAGAGCTT	TTCCCTATAA	TGTATGTGCG	TTGTTGCCCT	GAGAAAAGAC
52101	TGTAAAGATA	TTCTAAAAGA	AAATCAAGGA	AGAAAAATAT	TATAACAAGA
52151	ACACATCTTC	AGCCCAGACC	TCTCCCCCAA	ACTCTAGACC	TGGATGTCAG
52201	CTGACTGCTT	AACCTATCCA	GTTGGATGAA	AATAGACGTC	TCAAACCTCA
52251	CATGTATAGA	ATTGTTCCCT	TTCTTCCCTT	AAACATCCTC	TACTCTCAGC
52301	CTTTCTTATC	CCAGGTAATG	GGACCTCTAT	CACCTGTTGC	TAAGGTCTAA
52351	TAATGTGGAT	TCATCCTTAA	TTACTCTTCA	TACATACAGT	CAATATGTAA
52401	GGAAATCCTG	TTAGCTGTAC	CTTCAAATTA	TATTTAAGTG	TGACCTTTTC
52451	TCACCAACTC	CAGTGCTACC	ACCCTGGCCC	AAGCCATCTC	TCCCCTGGAA
52501	TACAGGCCCA	AAATCCTTTA	TCCAAATAAC	TTATGGAATA	TAGCATTTTT
52551	TAGATTTTAG	AAAATCAGTA	AGGTACACAT	ACTATATAGT	ACACACTGAA
52601	GTAGTGAAAC	ATGCTGATTT	TCCTCTAGTG	CTTTTACTGT	GAACGTATCA
52651	ATGTTAAGGA	AAGGAAAATG	ATATTAAGTC	AGAGATGATG	TCTCACAGCA
52701	TATATTTACT	AGCTTGACA	AATTTTTTAA	TGTTAGCAAG	ATTTAAGGCA
52751	AATTTTTTAC	TTATATTTTA	ATTGATCCT	ATGATGATTA	TTAAAGAAAA
52801	AAGTAGTTAT	CTCTAGAAAG	TATAAATTGA	GCTCTTGGCA	AATGTGAGCA
52851	AAACCAGAAA	TCAGATTTTT	TTAAAGTTAC	GTGTACATTT	GTCTATAGAG
52901	TTATAATTAA	AAGTATTGTG	CTCATAGCCA	GTCTGTGATC	TGGGGCATAT
52951	TATTATATCT	TCCTATGCCT	TAAAACAATG	TTTCTGTAA	GTATAAACAA
53001	AGTACCATTG	ACACTGCAGT	TTTTGTCCAT	TTGCTACTTC	CAAAAGAAAG
53051	GGGTACAAAA	CAGAAAAGTT	ATTTAAACTT	TAAGCAGTTG	GTTAGATATG
53101	GTAGTTATAA	TGAGCTTTGG	TATTTTAATA	TGGGGCTTAA	AAATTTTCAT
53151	CTAAACCAAC	ATTAATTATC	TAAGTGTGAT	ATCCTTAGGA	GGTCTTTGTT
53201	AAGTCCTCCC	AATTATATCC	AGCATCTCCA	AAGGTGACTG	AAGTCCCTTC
53251	TAATAACTCA	TCNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53501	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53551	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53601	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53751	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
53951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN

FIGURE 3R

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NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNTCATCCCA CCACTGGAGC ATTTTTCCTT
ATATTTAACC TAAATTTATG AAACACAGT TTATGCATTT TTAATATTGT
CAGATACTCA GGGTTAATGG ACACAGTTGT TCATTGTCTC CAGATCCCAT
ACTCCATGTA CTCAAAGACA CTTTCAGGAG ATGACTCACT CTTCCCTGGG
CCCNNNNNNN NNNNNNNNNN NNNNNNTTTC TTAGAAATGC TTTTTCCTCA
CCCACTTAGC AATCTTGTG ACTGGTCCTT TGAACATTCT TTATTTTCCA
AATCTGTCAC AAATGATCGA GTCAAAGATA TATAATAGTC AAATCTGACC
CAATACTGAT CACGGGGGGG TTTCTTTTAA CATGTTTGT AATCTAAATC
ATTTCTCTTT GTTGCAAAGT AGAGATTAT GGGCAGCTAT TTAATCTCCA
GATGTTTTTT CCTCAAANN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNTGGAATT TTATATTGGA TTTAATTTTT TTCATTCTAA
GTAATCCTTC ATATGCTTAA CTAGCTAAAT TTTACTTGTT GGTTCGTATA
TTCTTCCCTT AAATAATCAA AGTTAATTCA GATTATGGTT TTTTTCTTA
TCCTGATACA GCTTAATATA GCCATTGAAA ATATTCTCTA GAAAATTCTA
AGCTAATAT ACTTCTAAAT TTTAAGCATG AACTGAAAA ATAGTAAAA
GCATAGAAAA GGAATATGAA AATAGCATTG AAACATTTGG AATTAAGGGG
TTTTAACAC TACTAAAGAT AGAATATACT GAACCAGAAA ACCTAGTCTT
GATTTCTACC TCTATTTATG AGGTACATGA CTTTGGACTA GTATGAGTNN
NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
NNNNNNNNNN NNNNNNNNNN NNNNNNTCCC AGCTATCCTT TCTCACTGAG
TAGCTTCAAA GATCAGAGAT AAGGGATCTA GTGTTTGTGA ATTCTGAGTT
ACTATGAAAT GTAAAAGATT AATGTGTTTT GTTTATCACT GTAAATAACC
55401 TTGATGGGGA GAACCTATGT GATTTAAGGT TGCAACTTTT TTTGTGTGAT
55451 GTGAAATATT AAACATATTT TTAATAAAN NNNNNNNNNN NNNNNNNNNN
55501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
55701 NNNNNNNNNN NNNNNNNNNN AAAACAATT TTAGCTTGAG GGACCTAGG
55751 TTTTTTTAGG TTATATGACT AGAAATATAA TAAGATGTAT TTACAGGGCT
55801 AATCCGGTGG GCATGATTTG AGCAACACTA AAGTTATCTG ATGTAGCGTA
55851 AAATCTTGT TGTTCATTA ATGAGACAGA CTTGTGCTTC TCAAAGTGTG
55901 TTTTATAGAG CATTATTTCT CTGAAATATT ACACAGTTGT ATGTGTTAAA
55951 AAGTTCTTAG GTCAAATACA TTTAAGAACT CCTAGGTTTA GCTAAGTTAA
56001 ATAGGTTTCT TAACTGTAGG ACTTCTCAAT ACTCCAATGT GCTAACAATA
56051 TTGCAAAATCT CTAAGAGAGG CATATAATGT ATCTTTTCCC AAGTTGTTTT
56101 AACCATGGGA TTATTTGAAT CTTGGGATTA GAGTTTACTG GAATCAACTT
56151 TAGGTCAGGC TGGGCTAAAC TAGGAAGTAT GGAGACCATA CTCCACAAAA
56201 CCCAGTATCC CTCACTAGTT AGCTCTCGTT GCCTGGTTTT TGAGACTAAT
56251 GGGTTGATCT TAGATTTAGG AATGAGGGTT GGGGAGGGCA GAAAGGTGCT
56301 GCACAAACTT AGCCAGAAAA GCAGCCATAA GTGGTGGTAT GCCTGTATGG
56351 ACACCATAGG TTTGCTGCAG GGGATTGTTA AAAAGCCACT TTTCAAAGAC
56401 AAAACTCTGG TGTCACAGGG GTAGGAGCAA TCCCAGGGCA AAGAACTCA
56451 GAAAAACTTT CTGCAGAACC CAAAGTAAAG GAAGTTAGGG GGACATGCTT
56501 TCTGTTCTAG CAATATATAA TGAAATCTTA TATAACTATT AAACATGTTT
56551 TATGAAAAAT ATTTAATAAT TTTGAAAAAT ACCCATGTTA CAAAAATGTT
56601 ACCTGAAAAG TAGAAAGCTG TACCTGCCAT TTGACTCCAA TTAGATATAA
56651 AATACATGTC TGCATATGTC TGGATGTGTG TAAAAGTCTG AAAGAAAAAA
56701 GACCAAAATA GTAACCATGA GTATATCCTG TTTATGATAT TTTGGCGGAT
56751 TTTCAATTGTC TTTTGTGTTG CTTTATCCAG TAATTTTTTA ACTGTTCAAC
56801 TGTACTATCG TTGATAACAG TAATTCATTA TATCATTAAT TCCTTCAGAG
56851 AAGGGGCAGA GTAACAGAAC CCCACTCTTC TCAGCAGGAA AGTGAGGATT
56901 CTGATTCTTA ATCATGTTTA TTTTATTTTG GACATACTGA GTTTTAAAAA
56951 TTCATTGAAG GTTTTATTAA CTTCTATTTT TAACCTTTCA GATTTTCCTT

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FIGURE 3S

57001 TACAATTGAA TGTGATAGAT ATGTCCAATT TTAGCTAGGA AATTTGTATT
57051 ACGAGAGGGA ATATAACATC ACTTGGACCA GGAAACAGAT TTTTTTCCC
57101 CAGTGTTGTC AGAAGCCCAT TTAACTAAA ATAACATAGG ATGTTTATTA
57151 ACTAAAATAA CATAGGATGA TTATCTTAAG ATGTAGATTC CTAATCCTTA
57201 TGACACATTT ACTAAATCAG ACTTACTAGG GAAAGTATCT CTCAGTCTTT
57251 ATCNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57451 NNNNNNTCTG AGTAGGCACA CTAGTCCCC AACACTCAAC CTTTTATTCA
57501 ACCAGCGGTG AGCTGGATGT GAACATGACA GACCCAGTAG GGTTCCAATG
57551 CCTGACAACC TGCACCTGTC AGGAAGAGCC CCCTCCTTTC CTGCTCCCCT
57601 GCAACACATG GTTANNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
57851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN ATAGCAGGGC TCTTCTAAA
57901 GCATAATGGC AGCTCCAACC CAGCAGAACC ATATTCTGGA TGGAGTCAGA
57951 ACTAGCCAAA TGTAGGCTAT TTAAATATA GCAATTGTGC CTAGGCATGT
58001 GTCCACCTGA CTCATGTAAG ATAAAAAGAA AAGGCGTTAA TAGAAGCCAG
58051 ATTATAGAAG ATAATGTTAT TAATATGTAT CAGGTGCTCT TATGAGTGGC
58101 CATATCAGAG AACCAGCCTC ATTGTTGCTG TTATTACGCA ACATGAGACT
58151 GTGCTGCAAT TCCAAGTACC AAGCAGTAAG AAGAAAATTG TTTTCTTTTA
58201 CTGATTGCTG CATGTTGTCC TGAGGTTTTT CCCCTCATCT CTCTTCTACA
58251 GATTTTACAG AGTCTGTGGC TAGTTCAGTC ACATTGTTCT TAGTCATGGA
58301 AATATTATGG TCTTCTGAT TCTGTGTAGT GATAAGTAAA AAGATTGTTT
58351 CTGCTGAGGG GTGAAAAGGT CTTCAAAGTA GTTTGCTTTC TTGTAAACAG
58401 TAAGACCTG AGAGACCCTG AGAAGATGCC TGATATCTCC TTGAAAATTA
58451 AATTTCTGCT AGTGTTTTGA AGGAGCGAAT TGTCACCTCT CACAGGTTAG
58501 GATCTGCTGC TGTGAATTCT GAAAGTTTTT AAGATTTTTG ATTTATATTT
58551 TAATTAGATC CTATGGTAGC TAGTAAAGAA AATATCATTC TCTCCAAAAC
58601 GTATAAATGG GCCCTTGGTG ATTGTGACCA AAGTCAGAAG TCAGATTTTT
58651 TTTTGAAGTT ACATGCACAT TTGTCAATAG AGTTATAATT TACAAGTATT
58701 GTCCTCANNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
58851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTAC
58901 TATTGATGTT GAATTCATTT ATATAGTAAT GATAACATTT CCTACTTAAT
58951 TCATAAAAAG ACAGCCTATG CTGTTTTCTT GTTCTGAGTT TATATGTTTC
59001 TCATGCTTTT TATTATGGTT CATTACAATT TTAATGTTAT TTTTAACTAA
59051 CTAGATCCTT TTGAAACAAA TTGGTTTGCA AGTGTGAGCT GTTAGGTGCA
59101 CAGAGAAAAA TGAAAATAGA AACTTGCGAT TTTATTCTAG GCTTGTTACC
59151 AAATATTTAG AATACTGTGT TTTATTTAGG TGTTTATAGT CTCATTAGAC
59201 AGTTGTGATT TTAATAATAGA GACCACATCA TCTCAACTTC TTTACTGTGA
59251 AAATAATGAC AATAGTCTTT TCAGAGATGA ATCTGTCTAG ATGGGAAATT
59301 TACATGATTG ATCTGATGAG NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59351 NNNNNNNNNN NNNNNNNNNN NNNNNNNAAA ATAATCTGAC AAGTAGTTTC
59401 CCCAGAAAAT CTGATTTAGT AAATGTACCA AAAGGATTTA GAAATCTACA
59451 TCATAAATAA ACATTCTATG TTATTTTAGT TCAGACCCTA TTTTAATTCA
59501 GACTTCCTAT GGGATAAAAA CTTCCATTCT TTCTTTAAAT AGATTCTTTT
59551 GGCTTGAGTG CATTTACACC TGTCCCAAC AGCTGGTGGG CTCTGTCTCA
59601 CCCTAGACGG TGTTCTATGCT GCACTCAGTC CAAGCAGCCC TTATCAGAGA
59651 GTCTTCTTAC CACTTGCATT CTGGTGCGAA GGACTCATTC CTGGCAGAGC
59701 CTAACCTTCA TGGGAACCAT TGGCTTAGAA GAGAGGAGAA GNNNNNNNNN
59751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
59951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNTATCC

FIGURE 3T

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60001 TGTCTCCGGG CAGTGTCTCT GAGTCTTTCT AAAACTTTAT TAAAAGTTCC
60051 TACAAATACAT AAAAGAGAAA TAGGTATGTC ACAAAAATTG GGCTCATTGT
60101 TGATTAGCAA TGTCTATGCT CCACCTTTCA CCAGAGATTT AACTTTTTTG
60151 CCAATTTTGC TC'TTTACTGT CAGCCCAAAG GTGTCTGTGG AACTTTGTAG
60201 ATTCTTCCTA TGGGATGAAA GCTTTGACAA ACAAGGTCTT ATTTCTGTGA
60251 GTCCAACAAC CCTTTTCTTT TGGCTTATAA TGAATAGATG GCTAAAACCT
60301 TTCTCTAACA TGGTTAAAGA AATTTCAGAA ACTAATTTCC AGCCCTTTTA
60351 TTTGCTTTTC TCTCTGATCA CTTAAAATTG TGATGCATAT GTCCTGCATC
60401 TGTNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNCATC
60451 TCATAAAACT CTTGTCATTC ATCCCTACGC TCCAATCTGT GTCTCTAAAA
60501 GCCTCTAGGT TTTGCCACCA GAAACAGCCT TCAGAATATT GGAATAATTA
60551 CATATGTACC ATTCTCTTCA ATGAACTAAA CTCCTAAGCA TAGAAGTAAT
60601 TTAAGACAGT GTTATTTTTA ATCATTTAGT CCAACAACAA ATGCCAGAAC
60651 TGGCCTGGGT AATGCCATAG GAACCACCTT GTTTCCTATG AAACAGGAAG
60701 AGAATTTGCA AACCTACCTT TACTAAATAA TGCTTACATT TTGCTATAGT
60751 TACTCTTGGC AAGAAGTTGA GCAGTGGGAG GTGTATATGA TAATATTTAC
60801 ATTTACTTCT CTGTGCTTAC TGTTAATGTT TTCTGGGTAA AAATATGCAA
60851 TTGACTATTT GGGAAACTTC ATTTGTGAAC ACAGGTTATA TATGATCACA
60901 TCCCTGGGGA AAATACATAT TTAGTAGAAA GTGCCTGGCC AGCATTTCTT
60951 ACAAGAACTT TCCTGCTCCT TTTTGTGGCT GATTTTACCC CTGACTCCAG
61001 GGCCCGTAGT CCATTAGAAA GTACTGTGCT CCTCAGCCCA GTCCAACCAT
61051 GCCTTTATCC AGCTGTCACT TGCTTCAGTA CCTGTACATT CCCTTTCTTT
61101 TAGTTTATGC AGAAGGCTGT AAGAAGCAAC AGGCAAGACA TATCTTTTGG
61151 TGGGTAAAAC ATGGACCAAT GGTATAAAGA TTCTGGGGAC ATTTTCTAAA
61201 AATATATGAA CATTCAATGG TGATGTTAAT TTTAGTCATA ATTCCCCTAT
61251 GACACCCACT CTCACCTTCT TCCTGTTTCA TCTCCAAGCT ACTACCAGTA
61301 ATGGTCATTT CAGCATGCAA ACCTGATCTT GGCAATCCTC TGTTAATCCT
61351 TCAGAGGCCG CCAGTTTCCA CCAGGGATAA CGTCCAAAAT ATTTACAAGG
61401 CTTTAAAAGC TCCTGCACAC TCTGCTTCTA TCTCCAATTC CATTGATGCT
61451 CCTTCTCCT GCACCTTCTT GCTGCCTCCC TCCCCCTGTA AGGTCTACAG
61501 CAATTCTGAT GTTTCAGTCC CCTCTCTTTT CATTCTCCAG AGCCATAGCT
61551 CATAGTACTT CTTCTTATGT CATAGAGAAA GCATCACTTC TCAGAGATTT
61601 TTATGACGTG TATCCTCCCC AGCCTAGCTT AGCCAGTCCC TCACTCCCCA
61651 CTCCCGTACT CACTAGCATC CTCTGCTTCT TTAAAGCACA CATTACCTGG
61701 GGAAATTGTT AAAAATCNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
61751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
61801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNAATGAGT GGATGGAGTA
61851 GAAGGAGGCA GGATGCATGG ACAGATGGTG GAGGAATTGT ATTGCTAGCA
61901 CTTCTCTGAT TCTTTTFTAG TTTCTAAATT TATACCATT CTAATTCTAAG
61951 AATTAATGGT TCAACTGCAG AGAATAGCAG GTATGCATTT GTTTTATGA
62001 AATATATATA TTGTGTATTT AAGTTGAATA TTAGCCCAA GTATCAAGCA
62051 GGGGAAAGAA CAAATAGAAA AATCATGTAC CAATGCTAT TCTGGGNNN
62101 NNNNNNNNNN NNNNNNNNTT AATTAACATT TTCTGCATTG ATCAAAATAG
62151 CTCCCTTGAA ATCAAAGAAA AGTGTGTTGAA TTTCACAAAC ATATTTCAAT
62201 TTCATAGCCT TGCGTTCAAC AAGTATCAAG CCTATTCTAA GTTCTCTTTG
62251 AGTAACCAAA ATACAAATAA CAGACATATA ATTGCTATTT ATATGTGATC
62301 TAACAGAACC CTCTTTTATT TAGATGTCTT AGGTAAGTTT TTTATTCTA
62351 TTTATATTTT TTCTTTTAC AATCCTAAA ACATAGAATT ACAAAAAAAG
62401 TGAACCAATA CAAATGAAAA AAAAAATTTT ATTTCTAATA CTTAGATTAC
62451 CAATATTTAG CATATTGGCA TATTGGTGTA TTTATCCCTC TTTAGTCCTT
62501 TTTTTTTGGT TTGTGTTTCT TGTACATGAT TGTGATAATA ACATAATACT
62551 GCTTGAATGA TTTGTTCTGC TACTTATTTT ACTTAATATT TTCACATAAA
62601 CTCTAAAGTG TATCGGGGGT GGGTAGTTTT TTTTCTCTTG AAACCTCAGT
62651 GGGATGCTCT TAGTAATCCC ATACTGGTAT GTGTGAGGAA GGAAAATTAG
62701 TTAAATAATT TGGTATGGTT ATAGAGTAGA GCACACAAA TTGTAAGAAC
62751 CAATAGCTTC TGAGCACTTC TGGTCTCTAA ATTCTTGGA ATGTTTCCCA
62801 GTGGATTGTA ATGAAGGTAT ACATGATCAT CTGCTGCTAA ATTAAATGGT
62851 TCTTAGAAAC CAAGAACCNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
62901 NNNCATCTGA CATTTTACAA GTTGTTACTT GACTAATTCT TTGTGTTGCC
62951 ATCTTCTAAC TNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

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FIGURE 3U

63001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
63201	NNNNNNNACA	GGCTCCCGGT	GCCAGGAAAC	CTTTACATCA	ACACTCGATT
63251	TGCCATTTGA	TAGTCCTTCA	TCTGGGAGGA	AAAAAAAAGA	CGGAGGGGAG
63301	CTTGAAAAAC	TGTCATAATG	TCCCTGGAAT	ATGGTACTTT	TAAGAGTTGA
63351	GCCTATTCCA	TTTTGGAGAT	GATTTATATA	AGTTACAACA	AAAGAAGGGG
63401	ACAAAAACAT	GATTGTTCTA	TGGAGTTTTT	ATACTTTCT	GTCACAAGAA
63451	AGCACGCTTG	TCTACAATTT	TGTAATATTT	CTAGTAAATA	AAAGAGGCAC
63501	TCCCGCTCTC	AGAGACCAA	ATAAGGAAAG	TGTAATTGGA	TGTCATTGCT
63551	GTCAGTCAGC	TGGGCTATAA	AAGAGAGAGT	GGGGTTGCCT	CATCCCCTGG
63601	GTATCCACAG	TCAGCTGTGT	CCCTAGAGCT	TCTTTTCTTT	CATTGCTGCC
63651	CAGCTGGGTA	TATTGCAAGT	ATGGATTATA	AGAGGGGAAG	GGACTTCACT
63701	GTTTTAACGT	TTGAAACAAA	AAGGAAAAAA	CTCAGAAGTA	GTAAGCTAAA
63751	AACAACTTGT	GCAAACGTTT	TGGGATTATT	ACTTAATTTT	AAGAATTTTT
63801	GCTAAAAACA	ATAGGAACAT	CGTTGAAAAA	AGAACCCTT	TGAGTGATGA
63851	CTGTTTCATA	GTGTTCTACA	TCTCCTACTC	CCTGCCTTAT	AAAAATAAAG
63901	CTAATTAATT	GAAGTTCTGG	CAAAGAGAAG	GGAGTATTCC	TTGGCCTTTG
63951	ACCANNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64201	NNNNNNNNNN	NNNNNNNNNN	NNAATGATTT	AAAGAAATCA	ATTATTTTTT
64251	TAAAGTAGAT	TCTTATGCTT	TGTCCCACTT	GTGTCCTTTG	AGGAAAAGTG
64301	TGAAATACTA	CCTGGGGTTC	TAACAGGATC	TTTGNNNNNN	NNNNNNNNNN
64351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
64401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNA
64451	CACATGTGTG	TAAATAGCTG	CAATTCTTTA	TGAAAGTGTG	TAATAGGGGC
64501	TTATAAGCAT	GAACCTTGA	GGTACAAGAG	GGAAGAATTT	GATTCTGCCT
64551	GGGGCAGAAT	CACTCCACAG	AGGCCGTGAT	ATTTATGCTG	GGCCTTGAAG
64601	GAAGAAGAGA	TTTTTGGCAG	GTTAATTAGC	AGGAAAGAGA	GCATTGGGTC
64651	TGAGACGTGA	AAATGAATGG	CATGTTTGA	CAGCATTGTG	TATTTTGGTG
64701	GGGTAGATTG	TAACTCTGG	CCCAAGAAGT	TTGAGTTTGA	TCTTAAAGGA
64751	GCCAGGGAAA	CTGTTTAAAG	AAGGGAGGCC	ATGGTAGGAA	ATGTATATTA
64801	GAGTGCAACA	ATGTGCGGAG	TTCACTGGGG	GTGGGGAGTA	CATGCTGTGA
64851	TTAGAAACCA	AACCATTGCG	TTCCATCATA	GGTATTTTCA	GTTAAAACAA
64901	CCTTGATTTA	AAGATCATAA	TAATGTATCT	TTCGTAGAGA	TGAACCTTAG
64951	AATTTCATAG	AGATGAATAG	TTGGCTAGAA	ATTGGTTGCT	CTATTAAAAT
65001	GTATTTTCCA	GATAAAGACT	TTTTAAGTTA	TTTTTGTTGA	ATTTTAGAAA
65051	CTTTTGAAAA	TCATTTTAA	AAAATGTACC	CAGATCAAGG	TTGCAGTATA
65101	AATCACTGCA	GAACAAAATT	CGTGAATCTT	CATGTGATAT	ATAATTAAAT
65151	ATTTTGGATT	CATCCAGATG	AATAAAATGA	CTAGGCCTTT	TCCTCCTGCC
65201	CTTGTTAAAG	GTAATGCCTC	TTTATCAATA	CTTCACACAC	ACACACACAC
65251	AAAAACTCAA	AACCTTTCTC	TTGCAGTTCC	ACGCAACCT	TCAAATGACT
65301	TGTTTGAAAT	ATTTGAAATA	GAAAGAGGAG	TCAGTGCAGA	CGATGAAGCA
65351	AAGGATGATC	CAGGTGACAC	TTACACTCTT	AGTGCCATCA	TAATGACATT
65401	TTATTGTTTC	TCTCCATGAA	AATAACTTTT	AAATGTAGAT	CGTTTGGACC
65451	ATTTGGGAAA	ATTACACCTG	TTTTCTTTAA	CAACTCAGAT	TTTCTTTGTA
65501	GTAAATCAG	TTGAGCNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
65551	NNNNNNNNNN	TAGTACTTAA	ACTGTAAAAA	GGAAATCATA	TTTTATAAGT
65601	GATGATGTAA	CATTGTTATA	ATTTGGCAAC	ACTTGTGTGT	TCTATTTTTA
65651	CAGATGATGC	ACTATTGTGC	TGAGAAAAGA	TTAATGTAAT	TTCCCTTTGG
65701	TCTTATGGAA	AGAAGCTCTG	GTTATATGGA	TAGGAGAGAA	CACCTGTTGT
65751	CTAGATACCC	CTAGTTCATA	GATTCATTTG	TTGTTTTTTG	TTGATTTTCT
65801	GATCCACTCA	TCTTCTGAT	TATTCCTTGG	TAGGTGTTCT	GGTACACAGT
65851	TGTAATTTTG	ACCATGGACT	TTGTGGATGG	ATCAGGGAGA	AAGACAATGA
65901	CTTGCACTGG	GAACCAATCA	GGGACCCAGC	AGGTAAAACC	ATTTCAATTA
65951	ACTTTTTCTG	GTACACATTT	CAATGTGATA	CTATCTGAAG	ACTCCACTGC

FIGURE 3V

66001 TGCTAATCAA GTCTACTGTA ACACATCTCT GTGTTTACTT GATAAAGATG
66051 GTCAAAAAGG ACCATGCCTA GCATTTATAT TTCATTTCTT TGAAAGAGTT
66101 AAATTTGTGA GCTATCAACT AGCACTATAT TATGGGAGAC AAGTAGTTAA
66151 TTAAAAGGTC AACTAATTTT TCTCAAAAAG CTTGATAAAT AAAATATTTA
66201 GATTAATTCT TGCAAATAAT TCTTAAGTTA TTTGTAGCAC CCATTCCCAG
66251 GAATAAAAGA AGTAATATAG TGGTATATCA GCCATGGTAA TAGGCATTCC
66301 CCAGTTGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNAGAT
66351 TTGAGTGGTA GTAGAAGAAC ACAGTGGAAA TTTCTATAAA GTTGTGATTA
66401 TCCTCTGAAA AAATTTCTACT CTAACCTGGG TGCTGAAGGA AATGGTTACG
66451 AATCACCACC ACTCATTTTA TAACAAAAGG TAGATTTAGA CATAGTTCCT
66501 TGGAACTCAA AGGAGTTTTA AATTGCACAA TTCTATTAA TCTAAAGTTT
66551 TAGTACTCAT AAGACATCTT TTCTCTAGA TTCAAGATAG CTTTTCTCCC
66601 CTCAGTAGTT AAATCNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
66901 NNNNNNNNNN NNNNNNGAAG TTAAATCTTT TATGGATAAG GCCTACTTAA
66951 TGGAAAGGTG AGGAGTTTGG TTTCATTTTT TTTCTTTTTT ATACTCCTGA
67001 TTCTAGATTT TAAGAAGATA CAGAATGTGA AGGAAAAGCT TGTATTTCAT
67051 TTTATTTTAA AAGCCTAGTT CTTGAATACC ATACTGGATA AGAGACCAA
67101 ACACAGAAAA GTTAACCTGA GAGAGCTCAT GATATCTTAA ACCAGCTCEN
67151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
67201 NNNNNTCATG CATTCTAGC AGGCTCCCTG AAGATCTCTA TGGTGGTCCT
67251 CAACGCACAT TTTGAGTAAC AAGGTATTAA AAAATTAGTN NNNNNNNNNN
67301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
67351 NNNNNNNNNN NNNNATTTAC TTAAAAATTA AAATGTGAAT TAAATTCCTT
67401 AAAATAGGAA TATCAATAA ATTCCAAATT GGTTCATACA TTTCTTTTCA
67451 TTGTAAAAGA CAATATCATT TAGTGCCCTCA CACACAGTAC TCTCAGTCAT
67501 TCTTGCAATTA CTGTCTTACT CATTAAAGT TAACTCTGAG CAGGACAGCA
67551 TTATCATTAA TGTCACAGAT TCTGTGAATA AGAGAGAAAC CAACATATCT
67601 ACNNNNNNNN NNNNNNNNNN NNNNNTACAA TATAAAATAC CTATGACAGT
67651 CCTAGCTTAT TTAAATCTC ATCAATTTTA TTTAATTGTA GCAATTAATA
67701 TAAATTTATT TCATTGCTAC AGAGTTGTAG CAATTTACAC TCCTACCAAC
67751 AGTATTTGAA AACCATCCCC AACAGATATT ATAAAAGTAT TTTTTTAAAT
67801 CTCTACCAAT CTTATAGGTG AAAAGGAATC TCTTTTAATT TTAATTTGCA
67851 TTTCTTCTAT TGTGAAAAGT TGATCATGTT TTATCATTCA CTCGAGGAGC
67901 AAANNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
67951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
68001 NNNNCTCTGT ACTACTCATG CAGGCTCCTA GACAGTCCAA TACTCAGAAC
68051 ATCTGCAGCA TTATTGTGTT TTTGACTGTA CCACAGGCTG GCCTCAGTAG
68101 GTGTGCATGT GGTAGTGTGC ATGATCTGAT TAGCAGATCA CAGACCTGTA
68151 GATTAGACTG ACTGACCACT GACCTGGAGT AGTTTGCTAC AGAAGGAGGG
68201 ATCTTTGGCA GTCATGTATG ACAGAATGGT GAATAATATT TATGGTCATA
68251 ATGAATGATT CCTTCAAGTA AGTTACACTG GGGAGAGTAA TTCATGCTAA
68301 ACTCAGGAGA ATTCACTGCA CTTCTATGTA AACAATCTAT GTAAAATACT
68351 TGAGTTTTAG AATTTAAATA CTGTATTTTA GAACCAATTT AGTCCTTTTC
68401 AACATTTTTT TATTATTCAT TATATTTGTA AATGTTTAAA TTTGTTGTGA
68451 CCCAAATCTC CTTTCTCTC TGATGGAAAA ATGAGAAGAG GGTAGAAAT
68501 TAGAATGGTA GACAAAGAAA TTTGAAATCG TTATTGGACC GTGTTAGTAC
68551 AGAGCAAATT GAAAGGAAGA GATGCCTGCT TGAGTGATTG GATAACTCGT
68601 GATGATTGGC TACGGTCCCT GGAGGATGCT TTTCTAGAAT TGGTCCAAGT
68651 TTTTACCAAG AACTTAGATA AATAGGACAT TGAACCTAAT ATTGAAGATA
68701 AACTGACCAA ACTACGGTTG ACTCAAATCT GGAGAGGAAA GTGACTATGT
68751 GTGCTGATAC AACCAGCATT CGAAAAATTA GATTAATGGG TCACAATTAA
68801 GAAGGTGAAA TGTAATGGGG TTGACTCGAA GTTATGGCTC ATAGTCGAGA
68851 AACCAGTCAC ACATCTGAGT GAGGGGGAAG ACCTGACATA TCACTAAGGG
68901 TAGAAGACTT TAGAGTTTTA GTGTGTAATG AAATCAATCT AAGCGAACCT
68951 TGTGATGTTG CTGCCAGAAA TATGGACCAT CTCTATAGAA ATATGCTATG

FIGURE 3W

69001
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TTTCAAGAAT	AAAAATCCAC	TTTGGTTAAG	TGGTGAATCC	ACTTTTGAGA
ATTCTTTTTT	TCTAATATGA	GAAGAATAGA	GTTGGTCACT	TAGAAGAGGA
TGACCTGCAT	GGAAAGGTAT	CTCCAAGCTT	GTGAAAAACA	GGCAAAGGAA
CCATAACGTT	TAGCCTGGAG	AAGAAATGAT	GCATCAGGGT	TCCTTTTCAA
ATAATTGACT	AGGGTTAGAG	TTGTTCTCTG	TGACCGAAAG	GGGATGAGAA
TAGGATTGAT	GGGTAAAAAA	TACAGGGAGA	TTCATTTTGG	CTCACTGTCA
TCTAAAAAGA	GAACAGGCTG	ACATGGAAAG	AGTGAGTTAT	CTTGGTGGAA
GCATTTGACT	GGGTGACATA	TGGCAAGATA	CTGTTAAAAG	GTTTTGAGCA
TCAGATGAAA	GTTGGATTAG	AAAACCTCTA	AACCAGCTCT	GAGAGCCTGA
TTCAGAATGG	AATGTGGAAG	TAGTCCCAAG	AAATTCAGTG	AGCAGGATTC
TAGCTTGGA	AGAAGGATGG	GAAGACCAAA	AGATGGCAGA	GAGTTGGAAG
GCAGGATATG	TGAGGATGGA	ATTGCAGAAT	ATATTTTATG	AATATGTTGA
GAGAATTATA	ACCCAGCACT	GATGGGAAAA	TACTAATAAA	GCTTACCTTT
TCATGGTTTT	TTATTCTAGG	AAATTCAGGT	GGATGGANNN	NNNNNNNNNN
69701	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNTC
69751	ACATGTGAAG	GCCAGAGAAG	AATATAAAAA	ATCNNNNNNN
69801	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
69951	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70051	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	AATAATTTCT
70101	CTAATTACCA	AGCTAATTAT	TTACCTATTT	CTATCTAGAT
70151	ATAAAAGAAT	ATGTGTTTGG	ATATCCAATT	ATGGATGATT
70201	GCAGTTCTAA	TCCAAGATCC	AGATTTGTAA	ATATTCTTAT
70251	TTCTAAGAAA	ACTCTCAAAA	CTCAAAACCT	TAAGAAATAG
70301	AGTGCATTTG	CTAGCTGCCT	TTCATGGTGC	TATTAGGTTT
70351	AGTCACAGTG	AGATGTGAAA	TTAACAATGC	CTCTAAGAAA
70401	TGCTGCTGAC	AGACATGGTG	ATGCGCTGCA	GGTATGTAGC
70451	GGGACACACC	CTTCTCCTGT	GTGTGTCAAA	GCTAGAACTA
70501	CCTGGAACCT	TGATCTCTGG	AGAACAAGGA	TTAAGGGCAA
70551	ACTCTGTCTG	CCACTGATAG	CTACAAGGAA	TTTGCTTACA
70601	GTATGCCAGC	ATGTACATAC	AAGTATGTCT	ATTTCAGCAT
70651	TTTTAAAATA	CACATAAATG	TAAAATAAAT	CAACAATATA
70701	TTCTACCACC	CTGACTCCC	CATTCAACAC	CCAGCAAGAT
70751	TCCTGATTAT	GTTCTCAGAG	AGATATTTT	GGATACAATG
70801	CTGTGCCTTG	CCTTTGTAC	TTATCGATAC	TACCTTAAGA
70851	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
70901	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTGGGG
70951	CTATCCACTA	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71001	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNGC	TGAAGCATGT
71051	TACATACAGA	ACACNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71101	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71251	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71301	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71351	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
71451	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNTCAT
71501	TTTTTCTCTG	ATGTTCTTTA	TTTTTCTTTA	GTATTTTAT
71551	AAGTTTCTA	TACAAAAAGA	AAAATTATCC	TTTTTTAATT
71601	ATTTAAAAAC	ATTTTGTGTT	GTCTATTTTA	TGGTATTTT
71651	GCAAATTTGG	AACTTAAAT	GTTCTTCAGT	AAGAAATTGG
71701	ATTGGCATAC	TTGCAGCAAT	GCAAAGTGTA	TTTGCTACCA
71751	GTTATACAAG	AAGCAACTTA	CAACACTGCA	AATATAGTAT
71801	AAAAAAAGTT	CATATTCATG	TGCATTTATG	TGAATGTATT
71851	AGTTCAGAAG	TCAAACCTT	CACAAATACC	TCTAGATTTT
71901	AATTTAAAGG	CACCAACCAC	TACAGAATTA	AAAATAAATA
71951	TTATAACCCA	ACTTCTGGT	CAAGTTTTCG	AGCATCTATT

FIGURE 3X


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72001 CCTCCCCAAA ATTCTTGAGA TATTGTGATA CTGTAAACTG AATGAATGTT
72051 TAATATAATT GTACATTTAT CACCAGAATT ATGAAATCAG AAGTGAAAAT
72101 TTTAATAGGT AACTTGCTTG AACTGAATC AATTTTCCC TTAGTTAATG
72151 TTCCAAGTGG TATCATTTCC TTTATTACAA AGGGAACGAA TTCTTCATGG
72201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
72251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
72301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
72351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
72401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNTAC
72451 CTGTGATGAT TCAAAAGCTG ACTTATAGTG AGACATGTAA ATATTTTGGC
72501 CCAAAATATT GTTTGGATTA GTTTGTGGAG GAAGGGGACA AGGGAAGTGG
72551 GAGAAAGATT CTTAAGACAT TATGTATTTT TAGTGATTCA AGTACGTGAA
72601 TCAAGGATCT ATTTCCCTGC AGTTTTTTGC TGTATCCTTG GAACATCATT
72651 CGTTGATTCA AACATCCTTA AACACCTGCT GCCTGCTAGC AGGGTAACAC
72701 AGAGGTTTGG GGGAACTTT GGTTCAGACT TTTAAGTTGT TCACAACCTG
72751 CTGGGGAGCC CTTAGCACAG AGGCTGGCAC ACAGTAAGTG CACAGAAATC
72801 ACCTGTGACC TATAGAGCTC CGACGGGACT TGTTAGAGAA GACACTGGAA
72851 TAAAAAGTTA ATACCAATT TTATCATGTC CTGTATAAAT TAAGCATAAG
72901 AAAGAGATGA TAGTTTATAT CTGTTAACTG AAAACTAAAT GGGATTACTA
72951 CCAAAATAGA TACACATGTT CAACATTCCA ACCATTTTTT TATGGAAAAA
73001 CCAGTGGTTG AACATACAGT GTGTTTTT CAG TTGACTGAGA TAAATAGCC
73051 TGAGGGAATG TCATTTGTAC ATGGATCAAG TTTCAAATA CTACTTGCAA
73101 CTTTCTCTCT CTTGAGAAGC AGCACCCCC ACTTCACTGC TGCTTAACCA
73151 TTTTTTTTCT AATGCAGTTT CCTTAACAAC AGAGGGAAGA AAACCTGTGA
73201 GCCCTAGGGA TCTGAGAACA TCATCAAAGT GGTCTATCTA AAGTGAAAGT
73251 TTTTATTAAT ATTTGTGTTT ATGTATATAT AATAGGACAT ATTTATAGAA
73301 TAGATATGAT ATAGATTTGT TTTACTATAA AAATGTTTTA AATGGCTTAC
73351 CTCCAAATAA AATTGAAGCT CCAGGAAGAC GGGGAGGGT TCCTGAATAC
73401 CTCTGTATCT AACTTGGTGT AGATTTACAC CAGTGTGAGA AGCTCTGCCA
73451 ACTCTGATTT TTTTTTTAAA GAACCTTTAC GTTTAGAGAT TTTTTTTTTT
73501 TAAGTTGGGG GAGGAGAGAA TAAGCAGATA TAGGGCCCTT TAAATCACCA
73551 TCTGCTTTAC GTTTCAGAGG TTAATTATCC ACCAGAAAAT TCTCCCTAGA
73601 AATTTAGGGT CAGTTTTACC AAACCACCAA GCCAGATCGC CAGGGGTGTT
73651 GGACAACGTT ATCATAACT GGTGAGGGT ACAAGGTGGT GAATGTGTAT
73701 ATGTTGTCTG ATGCTATAT GTCTGATCAT ATTCCATTGG AAATATTCAT
73751 AGTGTTTGGT TACTAATTAT TGTGTGTCTC TGGCATTACT TGTACTTTCC
73801 ATGAGCAAAG TAAGTGAATG TTTTCTGTAA ACACATACCA TAGAACTTAA
73851 GACAGGCATA CAAATAAGTC ATATTTTCT TCTTCAAAA TCTGGGAATT
73901 CTTTACAAAG AAAAGAAAAA AAAAAAAAAA CTAAACTCC TGTCCATGCT
73951 GCTTGTTCTA GAAAGGGATA TTGGCACATA CACACAGCCC TGCTTTTCCC
74001 ATTCCAGGTG GACAATATCT GACAGTGTCT GCAGCCAAAG CCCCAGGGGG
74051 AAAAGCTGCA CGCTTGGTGC TACCTCTCGG CCGCCTCATG CATTACGGGG
74101 ACCTGTGCCT GTCATTCAGG CACAAGGTGA CGGGGCTGCA CTCTGGCACA
74151 CTCCAGGTGT TTGTGAGAAA ACACGGTGCC CACGGAGCAG CCCTGTGGGG
74201 AAGAAATGGT GGCCATGGCT GGAGGCAAAC ACAGATCACC TTGCGAGGGG
74251 CTGACATCAA GAGCGTAAGT AGATCCACAA AGGAGGCAGG ACCTGGGACG
74301 TTTTCCTTTC ATAGGAGAAC TCTGGGATCT GAATTTGAAG AAGCCTTGCT
74351 GTGTGAATTC AGGCTCAGAT AAAGGTTTGG GTTTTTTCT GGGCCTGATG
74401 ACTCCATTCA GTGTCTCTT CTGAAACCAC TTTCTGCTTC TTCATCCTTC
74451 TTCATTGCAA CCTGTGATCA CCACCTCTCC CTAACCCTGG TAAAGATCCA
74501 TTTTTTTTTA ATGGAAAAA AAATCTAGGA ATAGAAAAGT TTTTTTGGTT
74551 TTTTTTAAAG TTGATCAACA GAACTTCCA AGGGTGGGGT GGTGAGCTTA
74601 ATGTTCCTG CTTTCCCTTT CCTTTAATT CCTTAGATTT CAACTTTTA
74651 CTACCATAAA TTACCCAGGA GATGGTTCTT TTTCTTTTT TGAAATGTTT
74701 CTTTCAAGTT CAAATTTTT TCTTTGTTT AGAGATCACA GTTAAGCAGC
74751 GTAGGGTGGG AACTCAGAAC TACAATTGGA AAGCACTATT CTATTCAGGA
74801 CAGGATGTGG GAAGTGCTTT GATGGAATAT ATAAATTTGA TCTTAAGTAA
74851 TCAAGACATA GGTAAGCAAA AAATGGTCTA GGGCATCCCA ACAAATTAT
74901 GAATGCATTT GGGAAAATGT CATCATTTTG CTGGTGCTTA TGAACTTGC
74951 TGTTGGGAGA TACCTATGCC TGTATGTAGG TATAGTTTAT AAGAAACCAT

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FIGURE 3Y

75001 TTTAGAAAGA AAAGATAGAT TCCATTAATA CAGTTTTTAT CAGAGTACTT
75051 GGATTTTGTT TAATTCTTAC ATATTTTTTC TTAAAACTTT TCTCAGTATT
75101 TTTATTGTTT AGAGAAATAA AACAAGATAA TCATTTTAAA TCATAGCACT
75151 TACGTTTTCT CTTGTTTTAT AAGGAGCAAG GATGCTCTAT AGAAAATATA
75201 ATGTAAGAAT AATAAAAGTT TTTGGTTTTT ACATAGGTAA AGCAACAGTG
75251 TGATTGGATT ATGGTGTGTTG ATTCTATTCC ATTTTCAGCA AGAAAGCGAT
75301 GTTAACCACA AAGGAACTAA GAAACATTTA AGATAGGCTG TGTGATTATG
75351 ATCTTTTCAGA TCTTTGGCTC CTAATATCTG TTCCTTTATA TTCTATCACA
75401 CTCTTCTAAC TTTGGTAATC CTTGACAAAA GTGTGCACTT TATAAACAAAT
75451 CCTAAATCGA ATTGGTCTAT AGCTTAGAAT GGCTTTTTAA AGAATAATTG
75501 ATTCTGAGTA ATGTGGTCTG ATGAACAGTT TGATGACTTC AGTTTCTACT
75551 GAAAGAGAAG CTTCACTGAT ACTGGCAACT ATATTCTGTT TTTTTCCTCC
75601 TGCAAATAA GTTTAAATTT GGTTTGGGGG AAGGTTTGCC TTTATTTTTG
75651 CTTAATAAGG AGGCATTAGA AAGGGGCAGA GGAGGCTTGA CTGGTGTGTG
75701 CTTAGTCTCC CTAGGTCGTC TTCAAAGGTG AAAAAAGGCG TGGTCACACT
75751 GGGGAGATTG GATTAGATGA TGTGAGCTTG AAAAAAGGCC ACTGCTCTGA
75801 AGAACGCTAA CAACTCCAGA ACTAACAATG AACTCCTATG TTGCTCTATC
75851 CTCTTTTTCC AATTCTCATC TTCTCTCCTC TTCTCCCTTT TATCAGGCCT
75901 AGGAGAAGAG TGGGTCAGTG GGTGAGAAGG AAGTCTATTT GGTGACCCAG
75951 GTTTTTCTGG CCTGCTTTTG TGCAATCCCA ATGAACAGTG ATACCCTCCT
76001 TGAATACAG GGCATCGCA GACACATCAA AGCCATCTGT GGGTGTGCGC
76051 TTCCATCCTG TGTCTCTTTC AGGAAGGCAT TCAGCATGCG TGAGCCATAC
76101 CATCCTCCAT CCTGATTACA AGGTGCTCCT TGTAGCAAAT TATGAGAGTG
76151 AGTTACGGGA GCAGTTTTTA AAAGAAATCT TTGCAGATGG CTATGATGTT
76201 ATGTGTTCCG TGTTGTACCA TGAGTAGTAT TGAATCCCT TGAGATATGA
76251 TGTACAATGT GCTTGTGAAA TTGACTTACC CTCTTCACTT AAGTTAGTTC
76301 TGGCCTGACC TGAATCTGA CTTTTACTGC CATTCACCTT ATAAAATAAG
76351 GGTGTGTAAC ATATCAAGAT ACATTTATTT TTATCTGTTT TTTTTTCTC
76401 GTTAAAGACA ATTATGTAGA GTGGGCACGT AATCCCTCCT TAGTAGTATT
76451 GTGTTTTGTG TAAATGTGCT ATTGATATTA AGTATTTACA TGTTCCAAAT
76501 ATTTACAGAC TCTAGTTGCA AGGTAAAGGG CAGCTTGTTG TCTCAAAAAA
76551 ATACATGGTG AAATGTCATC CAGTTCCATG ACCTTATATT GGCAGCAGTA
76601 GGAAATTGGC AGAAGTGTTG GGTGTGGTA ACGGAGTGAT GAATTTTTTT
76651 TTAATGGCCT TGAGTTTGAT CTCTGCAAAG GATAGGAAAC CTTTAGGAAG
76701 ACAAGAAAGC GCAGTTAATT TAGAACTGTC ACTGTTTCAA GTTACACTTT
76751 AAAACACAG CTTTTACCAT CATAACATGG CTCTGGTAAT ATGTAGGAAG
76801 CTTTATAAAA GTTTTGGTTG ATTCAGAAAA AGGATCCTGT TGCAGAGTGA
76851 GAGGAAGCAT AGGGGGAAC TCCATTGGAA CAGATTTTCA CACAACGTTT
76901 TAAATTGATA TAAGTTTAGG CAGTTGTAGT TCATAACTTA TGTTGCTCAT
76951 GTTGTGCTGT GTCAGGATGG GATAGGAAGC AAGTCCCATG CTTAGAGGCA
77001 TGGGATGTGT TGGAAACGGA TTTACACACA CTGGAGGAGC AGGGCAAGTT
77051 GGAATTCTAA GATCCATGAA CCCCCAATG TATTTCTCCT CTGCATATTT
77101 TACCAATATA TTAaaaaaca ATGTAACCTT TAAAAGGCAT CATTCCTGAG
77151 GTTTGTCTTA ATTTCTGATT AAGTAATCAG AATATTTTCT GCTGTTTTTG
77201 CCAGGAATCA CAAAGATGAT TAAAGGGTTG GAAAAAAGA TCTATGATGG
77251 AAAATTAAAG GAACTGGGAT TATTGAGCCT GGAGAAGAGA AGACTGAGGG
77301 GCAAACCATT GATGGTTTTT AAGTATATGA AGGGTTGGCA CAGAGAGGGT
77351 GGCGAACGAG TGTCTCCAT ATGCACTAAG AATAGAACAA GAGGAACCTG
77401 GCTTAGACTA GAGTATAAGG GAGCATTCTT TGGCAGGGGC CATTGTTAGA
77451 ATACTTCATA AAAAAAGAAG TGTGAAATC TCAGTATCTC TCTCTCTTTC
77501 TAAAAAATTA GATAAAATTT TGTCTATTTA AGATGGTTAA AGATGTTCTT
77551 ACCCAAGGAA AAGTAACAAA TTATAGAATT TCCCAAAAGA TGTTTTGATC
77601 CTAAGTAGTAT TATGCAGTGA AAATCTTTAG AACTAAATAA TTTGGACAAG
77651 GCTTAATTTA GGCATTTCCC TCTTGACCTC CTAATGGAGA GGGATTGAAA
77701 GGGGAAGAGC CCACCAATG CTGAGCTCAC TGAATATCTC CTCCTTATG
77751 GCAATCCTAG CAGTATTTAA GAAAAAAGGA AACTATTTAT TCCAAATGAG
77801 AGTATGATGG ACAGATATTT TAGTATCTCA GTAATGTCCT AGTGTGGCGG
77851 TGGTTTTCAA TGTTCTTCA TGGTAAAGGT ATAAGCCTTT CATTTGTTCA
77901 ATGGATGATG TTTCAAGATTT TTTTTTTTTT AAGAGATCCT TCAAGGAACA
77951 CAGTTCAGAG AGATTTTCAT CGGGTGCATT CTCTCTGCTT CGTGTGTGAC

FIGURE 3Z

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78001 AAGTTATCTT GGCTGCTGAG AAAGAGTGCC CTGCCCCACA CCGGCAGACC
78051 TTTCC TTCAC CTCATCAGTA TGATTCAGTT TCTCTTATCA ATTGGACTCT
78101 CCCAGGTTCC ACAGAACAGT AATATTTTTT GAACAATAGG TACAATAGAA
78151 GGTCTTCTGT CATTTAACCT GGTAAAGGCA GGGCTGGAGG GGGAAAATAA
78201 ATCATTAAGC CTTTGAGTAA CGGCAGAATA TATGGCTGTA GATCCATTTT
78251 TAATGGTTCA TTTCC TTTAT GGTCATATAA CTGCACAGCT GAAGATGAAA
78301 GGGGAAAATA AATGAAAATT TACTTTTTCG ATGCCAATGA TACATTGCAC
78351 TAACTGATG GAAGAAGTTA TCCAAAGTAC TGTATAACAT CTTGTTTATT
78401 ATTTAATGTT TTCTAAAATA AAAAATGTTA GTGGTTTTCC AAATGGCCTA
78451 ATAAAAACAA TTATTTGTAA ATAAAAACAC TGTAGTAAT ACCAGTTGTC
78501 TATTCTTGTT TTTTGAGTTT TGTTTTTTTT TGA CTGGAA AAAAGCATTG
78551 AGGTAGTTAA ATGATGTTTC ACAAAGTCA TAGTAGAATC CCTTTTACTG
78601 TTTGGATGGT GGAACAAAG ATGTTGCCTG CAGTATTATA CTTTCTAGGT
78651 TATAAACAT GAGACACTTT ATTTTTTTTA TCAGCATGAA CAGGGAAAGA
78701 GATCAGAAGA TCACTATAAC CCATGCCATG CCTTAGTAAA TTGCTTTAGT
78751 TATGTTTAT TATCATTTCA TTGTAAACAT TTGCT (SEQ ID NO:3)

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FEATURES:

Genewise results:

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Start: 3000
Exon: 3000-3070
Exon: 5248-5348
Exon: 19533-19583
Exon: 34426-34518
Exon: 39701-39790
Exon: 44102-44221
Exon: 45394-45513
Exon: 47168-47302
Exon: 47607-47729
Exon: 49126-49127
Exon: 49132-49522
Exon: 65277-65363
Exon: 65834-65932
Exon: 74008-74264
Exon: 75715-75807
Stop: 75808

```

CHROMOSOME MAP POSITION:

chromosome 4

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
3365	C	T	Intron			
3411	G	A	Intron			
5243	G	A	Intron			
6532	T	G	Intron			
9208	-	G	Intron			
15833	T	C	Intron			
27795	G	T	Intron			
31341	A	G	Intron			
33370	G	A	Intron			
37788	G	A	Intron			
41465	C	T	Intron			
41466	A	G	Intron			
41653	T	G	Intron			
47666	G	A	Exon, coding	281	V	I
52613	G	A	Intron			

FIGURE 3AA

52645	G	A	Intron
59197	-	A	Intron
63508	T	C	Intron
75153	C	G	Intron
76017	C	G	Intron
76033	C	T	Intron
77194	A	G	Intron
77508	T	A	Intron
77557	G	A	Intron

Context:

DNA

Position

3365

CGGGAGGTGAGCTGGGCCCCGGGGCGCCCTCTCCTCCTTCCCGCGCTAATTTCACTCA
CTGTCTTGGGTCACTTTTCCCGCGGGTTTCGTGGTCAGAGAGGCGTCTCCTCCATCCA
GAAGTTGGGCCACCGCACAGCGTGGCGCGAGGAGAGCGGTCCAGCGGCTCCGAGTGCCCCG
CCCGAGGCGGAGAGGGCGCGCCCTTGCGAGTCTGGGACCCCATCCGCGCCCCCGAGGG
CGACTCGCCCCGGCTCGGGAATTAGGACTGAGGGAGAGAGCCGCTGGAGCCTGGGATCT
[C, T]

GGCTCTGAGGGCGCGGTTTAGCCACCTACGCCGAGGTGACGCGGAAACATCCCTTACCC
GGGAACTCCCGCGCCTGAAGTAGACGGCTCTTCACTGGGGAAGCTTCCAGGCCCGCGGG
GGGAGGCCCGGGCTCTGCTCAGGGCTCTCGGGGCGCTCACACAGAGAGTGGGTGCGAGT
CAGCGACTGGGCTACGGGGGAGATTTGTGGGCCTCTCCATTTGGTTTTCTTGAGGGAAGG
AGACTCAAAATGAGGACCGGAGGGTGGGCGCTCCGTGAATGTGAGCATGAGTGTGTGGAT

3411

TAATTTCACTCACTGTCTTGGGTCACTTTTCCCGCGGGGTTTCGTGGTCAGAGAGGC
GTCTCCTCCATCCAGAAGTTGGGCCACCGCACAGCGTGGCGCGAGGAGAGCGGTCCAGCG
GCTCCGAGTGCCCGCCCGAGGCGGAGAGGGCGCGCCCTTGCGAGTCTGGGACCCCATCCG
CGGCCCGCGAGGGCGACTCGCCCCGGCTCGGGAATTAGGACTGAGGGAGAGGAGCCGCT
GGAGCCTGGGATCTCGGCTCTGAGGGCGCGGTTTAGCCACCTACGCCGAGGTGACGCGCG
[G, A]

AACATCCCTTACCCGGGAACTCCCGCGCCTGAAGTAGACGGCTCTTCACTGGGGAAGCT
TCCAGGCCCGCGGGGAGGCCCGGGCTCTGCTCAGGGCTCTCGGGGCGCTCACACAGA
GAGTGGGTGCGAGTCAGCGACTGGGCTACGGGGGAGATTTGTGGGCCTCTCCATTTGGTT
TTCTTGAGGGAAGGAGACTCAAAATGAGGACCGGAGGGTGGGCGCTCCGTGAATGTGAGC
ATGAGTGTGTGGATGTGTGTGTGAGAGCGCACACACTGCGCCGCTCCTCAGACTCGGGCG

5243

GGCAGCCTTGAGAATTGTTGGTGTAGCTGGTGCTATTTCTACTTAAGAAAGCATCTTTC
CCTCCCGTTTTTTCTCCTACCCCTTGTGTGTTGGGGGATGGGGTATTTAACTGTCTGAAAT
TTGACATTAGATCATAGCAGAACTATTTCTGTGAAGGTGTTTTAACCTTAAATTTCTGCA
GGCATAAAAGAGTTTGTAGAAAATTGTTGGGTGTGGTTGACATTTTTTCTGAAGTAATAA
TACAGAGGAAATTACCTTCTCTCAAAAGTGTCCTTATTTATTTTGAATCTTTTTTTTTT
[G, A]

GTAGGTGGCCAGGCAAATAGTGTCATCGATTGGCCTATGTCGTTATGGTGGGAGGATTG
ACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTGAGCGTGAGTATCAAGCCT
GGGGACTTCAGTTCCCTGGGAGGTGTGGCTTCCACCTTGTTTCATGGCTTACCCACAT
ATCAGAGGGTTCACTAGCAAGGCTTGGCCTTGCAGGTCTGACTTGGGGATTTTCAG
GTACAGTCCAGACTCCTTATCTGCTTCTTTTCAGCTTTAGCCACCTGTATTACGGCCCA

6532

GGGCGGGGGTAGGGGGCACTTCTGGTAAGATGATGGGAACTAAGTTGGGTCTACATTGG
GATATATATTTTATTGCTAATGAGGAGGAGCTTAGAGGAAGAGAGAAGGGCAGTTACGA
AGGCTAGAGCTGGCAATGGAGAAGCCTGCCTTAGAGATGGGTTGCTAGTGTGAGGAGTCA
GGCAAATTTAAGTTTCAGGAAAGTTAGGAGTTCCTCTGCTATTTTAAATTTTGGAGGATGC
TTGCAATGTCTTCCTTAATTTTGTGAAAGAGGGACAGTGACAGTCACAGATTGACTCTAA
[T, G]

TGCACATAAAGACCACAATCTCTGGTTGGGAATAGAAAGGTAAGGAAATGAATGTTTGC
CTACCTGGTATGGAATTTGAGAACCAACAGATTCTAATAACCAAAATGTGAAGAAAGGAC
CCTTCTGTTGGCCCAACACACCTACACATAACCCCTCCTGAGTGAAAAATGAGTAGTTCTA
TACCTGCAGTCTCCAGCTGTGCAAATACTTCTGATACTACAGAAGACTAAATTCACCAG

FIGURE 3BB

GCACCATTCTTCTTTTTTGATCATCTTCCCTTAAACAATATTGAATAGACTAACCAGTG

9208 TCTGAGTTCCTTTGGCTGTCACTTGAGCAACTGTGGTTTCTGAAGGAAATTATGTGAATTA
GGATGGTTTTGTATCATTTATCCTTAAGAACAGGGAAAATTGAGATGTTTTCTTATGTTT
CTGCTGGAGATTTTGGAAAGATGTGAAACCTACACCTACAGATTGACCTTGCTTAGTTAG
CTCTGAACCTCCTGCTGCCTCTCCACGTAAAGTGAAAATTTGGATTCTTATCGGCTTC
AGATAAACTTACAGGTTAGTGAAACATAGGGACTGAGATATAGTAATTCATTCTGAAGCT
[-, G]
TTTTGGAGTGGTCAAATAATTTTAGTTGGATAATATATATTACTGGCTAATGATTGTGGA
TATTGGAAGTGATGAAAAAATTATTGAATTATTTCTTCTGCATTTCAAATGAAAAGGCT
ATTAGTTTGAGCAGAGAATTTTGATTTAGTAAACAAAATATTTAAATTTTCATGTTTCATT
TCTTCTCCTATCTGGGTTGAGATACTCAGTCTTATAAATGGAACATGATTATTTTTGTC
TCCCTAACTGGTTATTAACCTCCTGTCCATAATCACAAAACCTATATAGATTATATATTT

15833 CATACATTAGCTTTGGTAGATACTAGATGCCAGGGGAGTGCAAATTTGAGAATAAGGATT
TGGCATGGGTATTTGTCATGTTGAGAGTCAAGATTTAACTAAATTTTAAAACCAAACACT
TCATTTGATCAATATCTTTTAACCATCTGTAGATTAATAATATAAATCTCCAGAGCT
GACATTACTTTGCTATAACATCATCAGATCACAAGATTAGGGTTGCCTTTTGTAGATGTT
ATTCATTACTCTGAAATGTAGGAAATATGTCATCACAGTTTAAATTTGTAGTAATATA
[T, C]
ACAAAAGGAAAAACAACTAGGAATTTTGGATTTATGCTTACTTTGCCAAAAACCATGTT
GATTTTCAAAAACCTTTAGCC

27795 ATGAAAACAGAAAGAGAAAGTTAAATTTCAAGTAACTGAAAACAACAATAGTGCTCAG
AGGATTTTTTTTTAAGTGAAAAGGGATAGTGCTTAATTATGACAAATAAAAGCTAACTTG
AGATGCACATATACAGATGCAGCCACTTATTTTGGCGGGGACACTTCAGGAATTAATAAT
TTAAATAGCGAGAGATCAATAGATACTTGGTAAATGTGTCTGAATTGGATGTTCCGAGA
CACAAAAATAAAATGAGTTATTGACAGCTCTTGGGAGACAACATTATAAAGACTAGACAC
[G, T]
TTATTTATTTTAACTCTATGTTCTAAATTACCATTGAGTAATTGACATTCGTATTTGACT
ATGGTTTGTGGTTAAGTTCTTAATTGCAATAATGTTAAATAAAATGTGAAGCCCAAAGCA
AACAACAACAAAAATTATAGCAATACTTCAACAGAGGTAATAATAATATGCTGCATCAAT
GGTTTCAGAAATCCAGCATCTACATAAAACAAGCAACAGGGTAATGAAATTATTTTCTTTTC
AAATATTTCTGGCAGAGCTACTTTAGTTTTCTTAAGTTATAGATTGTGGTCTTAACTGCAA

31341 CCACTTTGCTTATATTCTGAAAGTCTTTTGTTCCTATTCCACTGCTCTTACCTCTAACA
CACTGCCTCTAACACACCAACCTGCAGTTGTAGTTATTACACACCCTCCTTGGTTCTTTTC
ATCTCTCTATCACAGCCCTTGTGTGGTTTAGCCAATATATTTTAGTTCCACAGCTAAAT
TTTCATACCCTCTATGACTCTCTAATCCCTGCCACACTTGCTTACTATAATACATTATA
TATATAACAAATGTTTGATACGTATTTATTGAATTCATTCCAGAACTAATGCCAGCAAG
[A, G]
TAACCTTTGTGCTATATAGGAGAATATCTTTTGTGCAACAGTTTCAAAGGGTTTTCTTT
TTCTAAGAAGAAAGAAATTGATTGTATCAACTTTATGAGTATCCTACCGCATTTAATAGC
CATTGGCTAATCTAAGGGTTCCTGGTTACTTCACTGAATAGCCTATCAGATGGAAGTGCA
AACAACAGTTTGTGTTTGAATAGGACTCCCTAAACATGGAAGAAACATTACAGTGTTGG
CCTGTTGGAATGTGTGCATTGATGTGCTCAAGATTAGGGCACTCTGCTTGAGAACAAAT

33370 CCACTCACCTGATTGTTTCTCACTCTTCCCTCCACCATTTACCCATCTCTTTAGCTTAATG
AGTCCCCTGTGTATCTCCCACTAAACAGCGGCTTACTTGCTGTGAAATATTCTTCTCT
TGGGTAGTCTGCTCCCTTCTCTGTCTACTCATGCTTCAAGATTCAACATAAGCCTCCTCT
ATGAGGCTTTCTGCACGTATGTATATGGATTGCTTGTGTAATGATTTCTTCACAGATTT
CATATTGCTGATAAATAAATATTGTTTTGAATAAGAAACGTGGTTTTGTATTTTTATCTC
[G, A]
ATTGTAGACTCCTTGAGACCAGTACCATGCTATACAATTATTTTTCATCTATTATAGTGT
CTGGCATAGGGACATGCACATATTTGGTACAGAA

37788 GCCCTGTCAGGATCAGGGAAGCTGCCATGTGTGGCCTGGTTGAGTGTGAGAGCTGCCTAG
AGACTTCCATAAAAAGTTGTTAGAGAAAATTGTTGATAGTGCCTACATAGCAGATTAACCT
AAACTGTTTTTCATTACAGGCCACACATTTTAATAAAGTAGAAAATATGCTTCACAGATAA
GGGAAATCAACAGGCTCCTTTTTTCTGGAGGAGAGAAATGTCAAAAAGAAATTAATTTTG

FIGURE 3CC

AAATAACTTTACAGAACTGGAAATTAGCTTTTGATTAAGTAGCTTTTGGTATATGACA
[G, A]
GTATTCACTGAGAATTTTGTAGCGAGTTATATACTTTAAGAAATAACCCCCAGAACTTG
CATCATGGTGTAAACAGCTTGAATAAACAAGTGCTTAACCACTGCCTTTAGAGCTGCCTG
GGAAACAGCCAGAATACCAGGGCAAGCTGCATTTTGGAACTGGTTAATTTAGTAGCCTT
GCCACAGGCTTAGTGTGATCTGCTTTTGGTGGCTTGATCTTCCCCACTAAGTCATTTTCT
GGATTTGTTACACCTAGAACTGTTAGGAAATTACAGGCTTGGGCTGATCATTAACATACT

41465 TTTATTTCTAGGTTCTTTTATCAACTTTTAAGATTTATTTGAGACAGTATGATCAATGAC
TTCATTTTGTCTGCTTATTTATGTAGGAGTATTTACTATAATTTGGAAGTAATTTATTT
TTGAATTTATTGCTTAATTGAATGATCTCCAATAGATTGTGATAATGAACACAGCATTTA
TAGAAAGCAGCACATATTAACCTTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTA
ACATAATTGAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGA
[C, T]
ACCAGATGCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGTCTGATATTTGGCAAA
TTTTGATAAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATA
AGGGTCATTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAG
TCACTAGTGATATTAACACCAGTCAGCTGTCAGGGAATATCATCCAGACCATCAGCAGCT
GGTAGAGTACAGCTTTCTCAATTGCTTTCCATGTTTTGGATACTTATATGCCCGTTAATA

41466 TTTATTTCTAGGTTCTTTTATCAACTTTTAAGATTTATTTGAGACAGTATGATCAATGACT
TCATTTTGTCTGCTTATTATGTAGGAGTATTTACTATAATTTGGAAGTAATTTATTTT
TGAATTTATTGCTTAATTGAATGATCTCCAATAGATTGTGATAATGAACACAGCATTTAT
AGAAAGCAGCACATATTAACCTTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTA
CATAATTGAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGAC
[A, G]
CCAGATGCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGTCTGATATTTGGCAAT
TTTGATAAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATA
GGGTCAATTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAGT
CACTAGTGATATTAACACCAGTCAGCTGTCAGGGAATATCATCCAGACCATCAGCAGCTG
GTAGAGTACAGCTTTCTCAATTGCTTTCCATGTTTTGGATACTTATATGCCCGTTAATA

41653 AGCACATATTAACCTTACTTAATATGGCACTAGGTCAATGAGAAAAGAAGGTAACATAATT
GAAGACAAGAACTCTTAAGAAAACCTGAGGACAAAAAGGCTTCTCACCAGGACACCAGAT
GCATTTAATCTTTTGAAGCTCTGTACTTTAGGAAAAGTCTGATATTTGGCAATTTTGAT
AAACATGGATGACTATGGAATCCTATTTTATAGTATCTGAAGTGGCTTTCATAAGGGTCA
TTGTGAAGTTTGTAGGAGACACCTGCCTGTGGCAGATGGGACAATGATGGCAGTCACTAG
[T, G]
GATATTAACACCAGTCAGCTGTCAGGGAATATCATCCAGACCATCAGCAGCTGGTAGAGT
ACAGCTTTCTCAATTGCTTTCCATGTTTTGGATACTTATATGCCCGTTAATAACAGGTAA
AATAGCCAGTACATCATTCCACATTTACCCATTGAATGTTGCATGTTTTCTTCTTTCC
CATATTCATACAGTCCAGATTTTGTGGACTCATGACAGCACATTGGCTTTTCTTTCC
TTTCAGTTTCATGATTCTTAACCCCAAGTGCTTTTGCCATGGGAACGGAAGGATAAATT

47666 GTGGTGATGGCTGGAATGTCAGGGGCAGGGGAGAGTACTGGCGTTAAGTTAAACCAACAG
ACATCCAGTTTAAACCACTGGTAGTTCTCAGTCTACATGTAGTTTATTTCTTCTGTTTATC
TGCCAATTTTATGTAGATCATCACATTGCCAAAAAAATCATTTTGAAGCTGTATATAT
TTTTATGTGCATCATATTTATCTCCTAAATAAGTCTCTTCTTTCTTCTTCTGATGCA
GACATAGCAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTGATGTTATAAC
[G, A]
TACGTGGGTCTACAAGTGCAAATGTAAGAAGGATACCAGGGTGATGGACTGACTTGTG
TGTGTGAGTAGCACTTGTCTCTCAGCTTTAAATTCTAGCAGGAAATACAGGATTACACAA
AGGCCATTGCTAGGGAAAATAAGGAATAAGATTATCAAAGAAGTATAATTGTCATAATTG
GTTATATTTGCTTTGATTTCCACAAACAATAAAATCACTTGCTCAGGTAATTTGTAAGAA
CTAAGGACTCAGTAATACACTATAATCTTAAGAGTATTTAATCTCTTCACTGAAATCTC

52613 AGGTAATGGGACCTCTATCACCTGTTGCTAAGGTCTAATAATGTGGATTCACTCCTTAATT
ACTCTTCATACATACAGTCAATATGTAAGGAAATCCTGTTAGCTGTACCTTCAAATTATA
TTTAAGTGTGACCTTTTCTCACCACCTCCAGTGCTACCACCTGGCCCAAGCCATCTCTC
CCCTGGAATACAGGCCCAAAATCTTTTATCCAAATAACTTATGGAATATAGCATTTTTTA

FIGURE 3DD

GATTTTAGAAAAATCAGTAAGGTACACATACTATATAGTACACACTGAAGTAGTGAAACAT
 {G, A}
 CTGATTTTCCTCTAGTGCCTTTACTGTGAACGTATCAATGTTAAGGAAAGGAAAAATGATA
 TTAAGTCTAGAGATGATGTCTCAGCATATATTTACTAGCTTGACAAAATTTTTAATGT
 TAGCAAGATTTAAGGCAAATTTTTACTTATATTTAATTGGATCCTATGATGATTATTA
 AAGAAAAAAGTAGTTATCTCTAGAAAAGTATAAATTGAGCTCTGGCAAATGTGAGCAAAA
 CCAGAAATCAGATTTTTTTAAAGTTACGTGTACATTTGTCTATAGAGTTATAATTAAAG

52645 GTCTAATAATGTGGATTCACTCTTAATTACTCTTCATACATACAGTCAATATGTAAGGAA
 ATCCTGTTAGCTGTACCTTCAAATTATATTTAAGTGTGACCTTTTCTCACCAACTCCAGT
 GCTACCACCTGGCCCAAGCCATCTCTCCCCTGGAATACAGGCCCAAAATCCTTTATCCA
 AATAACTTATGGAATATAGCATTTTTTTAGATTTTAGAAAAATCAGTAAGGTACACATACTA
 TATAGTACACACTGAAGTAGTGAAACATGCTGATTTTCCTCTAGTGCCTTTACTGTGAAC
 {G, A}
 TATCAATGTTAAGGAAAGGAAAAATGATATTAAGTCTCAGAGATGATGTCTCAGCATATAT
 TTACTAGCTTGACAAAATTTTTAATGTTAGCAAGATTTAAGGCAAATTTTTACTTATA
 TTTTAATTGGATCCTATGATGATTATTAAGAAAAAGTAGTTATCTCTAGAAAAGTATAA
 ATTGAGCTCTTGCAAATGTGAGCAAAACCAGAAATCAGATTTTTTTAAAGTTACGTGTA
 CATTTGTCTATAGAGTTATAATTAAAGTATTGTGCTCATAGCCAGTCTGTGATCTGGGG

59197 CTACTATTGATGTTGAATTCATTTATATAGTAATGATAACATTTCTACTTAATTCATAA
 AAAGACAGCCTATGCTGTTTTCTTGTTCTGAGTTTATATGTTCTCATGCTTTTTATTAT
 GGTTCATTACAATTTTAATGTTATTTTTAACTAACTAGATCCTTTTGAAACAAATTGGTT
 TGCAAGTGTGAGCTGTTAGGTGCACAGAGAAAAATGAAAAAGAACTTGCATTTTTATT
 CTAGGCTTGTACCAAATATTTAGAATACTGTGTTTTATTAGGTGTTTATAGTCTCATT
 [-, A]
 GACAGTTGTGATTTTTAAATAGAGACCACATCATCTCAACTTCTTTACTGTGAAAAATAAT
 GACAATAGTCTTTTCAAGAGATGAATCTGTCTAGATGGGAAATTTACATGATTGATCTGAT
 GAGNN
 AAAATAATCTGACAAGTAGTTTCCCAGAAAAATCTGATTTAGTAAATGTACCAAAAGGAT
 TTAGAAATCTACATCATAAATAAACATTCTATGTTATTTTAGTTTCAAGCCCTATTTTAAT

63508 ACAGGCTCCCGGTGCCAGGAAACCTTTACATCAACACTCGATTTGCCATTTGATAGTCCT
 TCATCTGGGAGGAAAAAAGACGGAGGGGAGCTTGAAAACTGTCAATGTCCCTGG
 AATATGGTACTTTTAAGAGTTGAGCCTATTCCATTTTGGAGATGATTATATAAGTTACA
 ACAAAGAAGGGGACAAAAACATGATTGTTCTATGGAGTTTATAACTTTCTGTACAA
 GAAAGCACGCTGTCTACAATTTGTAATATTTCTAGTAAATAAAGAGGCACTCCCCGT
 {T, C}
 TCAGAGCACAAATAAGGAAAGTGTAATTGGATGTGCTGTCAGTCAGCTGGGCTAT
 AAAAGAGAGAGTGGGGTTGCCTCATCCCCTGGGTATCCACAGTCAGCTGTGTCCCTAGAG
 CTTCTTTTCTTTCATTGCTGCCAGCTGGGTATATTGCAAGTATGGATTATAAGAGGGGA
 AGGCACTTCTGTTTTAACCTTTGAAACAAAAAGGAAAAAAGTCAAGTAGTAAGCTA
 AAAACAACCTGTGCAACGTTCTGGGATTATTACTTAATTTTAAGAATTTTGCTAAAAA

75153 AAGACATAGGTAGCAAAAAAATGGTCTAGGGCATCCCAACAAAATTATGAATGCATTTGG
 GAAAATGTCATCATTTTGTGCTGCTTATGAAACTTGCTGTTGGGAGATACCTATGCCTG
 TATGTAGGTATAGTTTATAAGAAACCATTTTAGAAAGAAAAGATAGATTCCATTAATACA
 GTTTTTATCAGAGTACTTGGATTTGTTTAAATCTTACATATTTTCTTAAACTTTTC
 TCAGTATTTTATTGTTTAGAGAAATAAAACAAGATAATCATTTTAAATCATAGCACTTA
 {C, G}
 GTTTTCTCTGTTTTATAAGGAGCAAGGATGCTCTATAGAAAATATAATGTAAGAATAAT
 AAAAGTTTTTGGTTTTTACATAGGTAAAGCAACAGTGTGATTGGATTATGGTGTGTTGATT
 CTATTCCATTTTCAAGCAAGAAAGCGATGTTAACCACAAAGGAACTAAGAAACATTTAAGA
 TAGGCTGTGTGATTATGATCTTTCAGATCTTTGGCTCCTAATATCTGTTCTCTTTATATTC
 TATCACACTCTTCAACTTTGGTAATCCTTGACAAAAGTGTGCACTTTATAAACAATCCT

76017 CGTCTTCAAAGGTGAAAAAAGGCGTGGTCACACTGGGGAGATTGGATTAGATGATGTGAG
 CTTGAAAAAAGGCCACTGCTCTGAAGAACGCTAACAACCTCCAGAACTAACAATGAAGTCC
 TATGTTGCTCTATCCTCTTTTCCAATTCTCATCTTCTCTCTCTCTCTCTCTCTCTCTCTCT
 GCCTAGGAGAAGAGTGGGTCACTGGGTGAGGAAAGTCTATTTGGTGACCCAGGTTTTT

FIGURE 3EE

CTGGCCTGCTTTTGTGCAATCCCAATGAACAGTGATACCCTCCTTGAAATACAGGGGCAT
[C, G]
GCAGACACATCAAAGCCATCTGTGGGTGTTGCCCTCCATCCTGTGTCTCTTTCAGGAAGG
CATTACAGCATGCGTGAGCCATACCATCCTCCATCCTGATTACAAGGTGCTCCTTGTAGCA
AATTATGAGAGTGAGTTACGGGAGCAGTTTTTAAAAGAAATCTTTCAGATGGCTATGAT
GTTATGTGTTCCGGTGTGTACCATGAGTAGTATTGACTTCCCTTGAGATATGATGTACAA
TGTGCTTGTGAAATTGACTTACCCTCTTCACTTAAGTTAGTTCTGGCCTGACCTGAACTC

76033 AAAAGGCGTGGTCACACTGGGGAGATTGGATTAGATGATGTGAGCTTGAAAAAGGCCAC
TGCTCTGAAGAACGCTAACAACCTCCAGAATAACAATGAACCTCCTATGTTGCTCTATCCT
CTTTTTCCAATTCTCATCTTCTCTCCTCTTCTCCCTTTTATCAGGCCTAGGAGAAGAGTG
GGTCAGTGGGTGAGAAGGAAGTCTATTTGGTGACCCAGGTTTTTCTGGCCTGCTTTTGTG
CAATCCCAATGAACAGTGATACCCTCCTTGAAATACAGGGGCATCGCAGACACATCAAAG
[C, T]
CATCTGTGGGTGTTGCCCTCCATCCTGTGTCTCTTTCAGGAAGGCATTACAGCATGCGTGA
GCCATACCATCCTCCATCCTGATTACAAGGTGCTCCTTGTAGCAAATTATGAGAGTGAGT
TACGGGAGCAGTTTTTAAAAGAAATCTTTCAGATGGCTATGATGTTATGTGTTCCGGTGT
TGTACCATGAGTAGTATTGACTTCCCTTGAGATATGATGTACAATGTGCTTGTGAAATTG
ACTTACCCTCTTCACTTAAGTTAGTTCTGGCCTGACCTGAACTCTGACTTTTACTGCCAT

77194 AACGTTTTAAATTGATATAAGTTTAGGCAGTTGTAGTTCATAACTTATGTTGCTCATGTT
GTGCTGTGTAGGATGGGATAGGAAGCAAGTCCCATGCTTAGAGGCATGGGATGTGTTGG
AACGGGATTTACACACACTGGAGGAGCAGGGCAAGTTGGAATTCTAAGATCCATGAACCC
CCAAGTGTATTTCTCCCTGCATATTTTACCAATATATTAACCAATGTAACCTTTTAA
AAGGCATCATTCCTGAGGTTTGTCTTAATTTCTGATTAAAGTAATCAGAATATTTTCTGCT
[A, G]
TTTTTGCCAGGAATCACAAAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAAAA
TTAAAGGAAGTGGGATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTTGATG
GTTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGC
ACTAAGAATAGAACAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGC
AGGGGCCATTGTTAGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTC

77508 TCACAAAGATGATTAAAGGGTTGGAAAAAAGATCTATGATGGAAAATTAAAGGAAGTGG
GATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTTGATGGTTTTCAAGTATA
TGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGCACTAAGAATAGAA
CAAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAGGGGCCATTGTT
AGAATACTTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTTCTAAAAAA
[T, A]
TAGATAAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAAGGAAAAGTAACA
AATTATAGAATTTCCCAAAAGATGTTTGTATCTACTAGTAGTATGCAGTGAAAATCTTT
AGAACTAAATAATTTGGACAAGGCTTAATTTAGGCATTTCCTCTTGACCTCCTAATGGA
GAGGGATTGAAAGGGGAAGAGCCCAAAATGCTGAGCTCACTGAAATATCTCTCCCTTA
TGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAATGAGAGTATGAT

77557 AAAGGAAGTGGGATTATTGAGCCTGGAGAAGAGAAGACTGAGGGGCAAACCATTTGATGGT
TTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCGACCAGCTGTTCTCCATATGCAC
TAAGAATAGAACAGAGGAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTTGGCAG
GGGCCATTGTTAGAATACCTCATAAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTC
TTTCTAAAAAATTAGATAAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCCAA
[G, A]
GAAAAGTAACAAATTATAGAATTTCCCAAAAGATGTTTGTATCTACTAGTAGTATGCAG
TGAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGGCATTTCCTCTTGAC
CTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCCTAGCAGTATTAAAGAAAAAAGGAACTATTTATTCCAAAT
GAGAGTATGATGGACAGATATTTTAGTATCTCAGTAATGTCTAGTGTGGCGGTGTTTT

FIGURE 3FF